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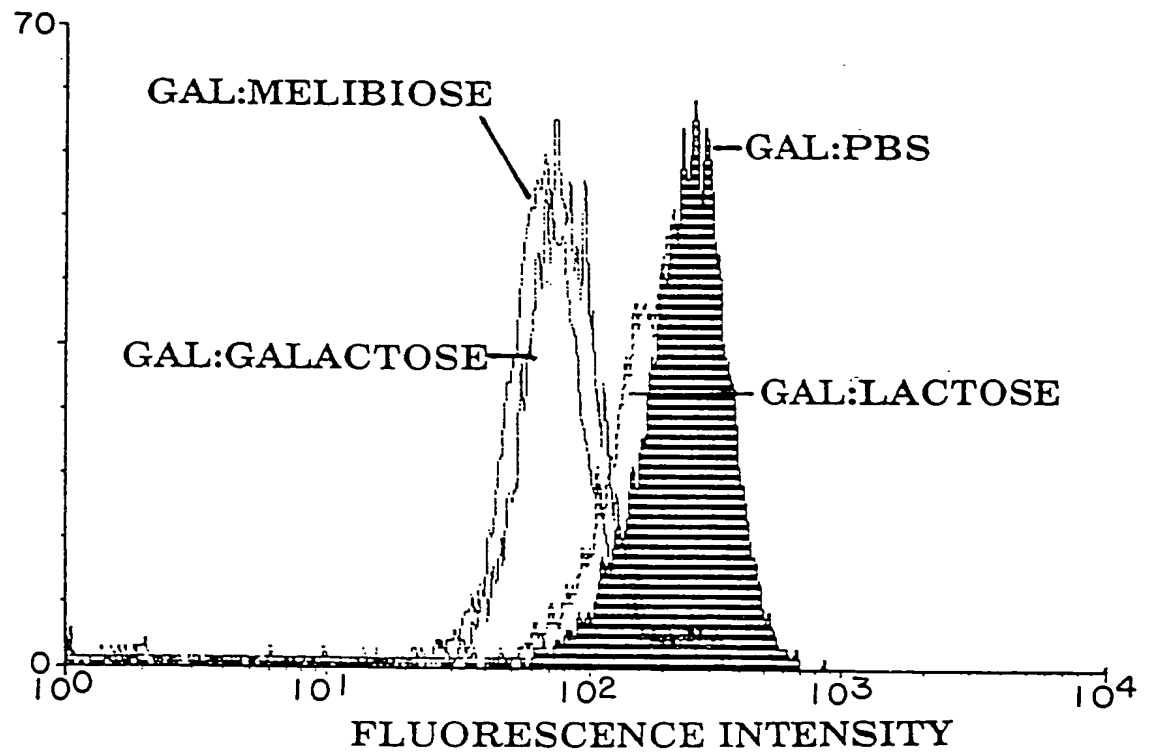


FIG. 1

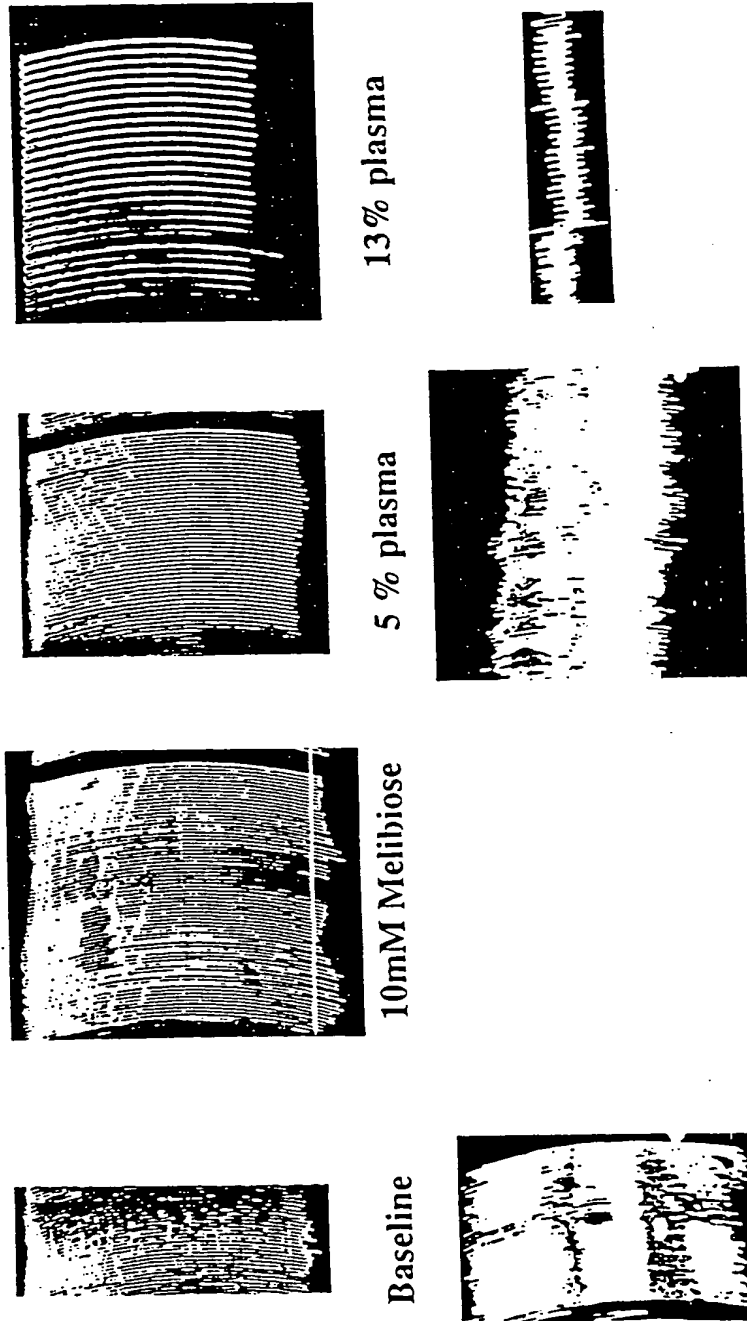



FIG. 3

PGTCD	351	-----	-----	-----AGC	CCTGCCCTCCT	TCTGCAGAGC	400
BOVGSTA	351	AAGGCTGCAC	CTTCGCTTCC	TCCC---AGC	CCTGCCCTCCT	TCTGCAGAAC	400
MUSGLYTNS	351	AACCCTGTAC	CTTCCCTTTCC	TCTGCTGAGC	CCTGCCCTCCT	TCCGCCAGGCC	400
PGTCD	401	AGAGCTCACT	AGAACTT-GT	TTC-----GCC	TTTTTACTCTG	GGGGGAGAGA	450
BOVGSTA	401	GGAGCTCAGT	AGAACTT-GG	TACTTTTGGC	TTTTTACTCTA	GGAGGAGAGA	450
MUSGLYTNS	401	AGAGCTCGAC	AGAAGCTCGG	TTGCTTTGCT	GTTTGCTTTG	GAGGGAACAC	450
<div> <div>Exon 2</div> <div>Exon 3</div> </div>							
PGTCD	451	AGCAGAGGAT	GAG-----	-----	-----	-----	500
BOVGSTA	451	AGCAGACGAT	GAG-----	-----	-----	-----	500
MUSGLYTNS	451	AGCTGACGAT	GAGGCTGACT	TTGAACTCAA	GAGATCTGCT	TACCCCAAGTC	500
PGTCD	501	-----	-----	-----	-----	-----	550
BOVGSTA	501	-----	-----	-----	-----	-----	550
MUSGLYTNS	501	TCCTGGAATT	AAAGGCCTGT	ACTACCTTGC	CTGGACCCTAA	GATTTTCATG	550
PGTCD	551	-----	-----	-----	-----	-----	600
BOVGSTA	551	-----	-----	-----	-----	-----	600
MUSGLYTNS	551	ATCACTATGC	TTCAAGATCT	CCATGTCAAC	AAGATCTCCA	TGTCAAGATC	600
<div> <div>Exon 3</div> <div>Exon 4</div> </div>							
PGTCD	601	-----	-----	-----	-----	---GAGAAAA	650
BOVGSTA	601	-----	-----	-----	-----	---GAGAAAA	650
MUSGLYTNS	601	CAAGTCAGAA	ACAAGTCCTC	CATCCTCAAG	ATCTGGATCA	CAGGAGAAAA	650
PGTCD	651	TAAATGAATGT	CAAAGGAAGA	GTGGTTCTGT	CAATGCTGCT	TGTCTCAACT	700
BOVGSTA	651	TAAATGAATGT	CAAAGGAAGA	GTGATTTCTGT	CAATGCTGGT	TGTCTCAACT	700
MUSGLYTNS	651	TAAATGAATGT	CAAAGGAAGA	GTAATCCTGT	TGATGCTGAT	TGTCTCAACC	700
Start							

FIG. 4B

PGTCD	701	GTAATGGTTG	TGTTTTGGGA	ATACATCAAC	AGCCCAGAAG	GTTCTTTGTT	750
	701	GTCAATTGTTG	TGTTTTGGGA	ATATATCCAC	AGCCCAGAAG	GCTCTTTGTT	750
	701	GTGGTTGTCG	TGTTTTGGGA	ATATGTCAAC	AGCCCAGACG	GCTCTTTCTT	750
<div> <div>Exon 4</div> <div>Exon 5</div> </div>							
PGTCD	751	CTGGATATAC	CAGTCAAAA	ACCCAGAAGT	TGGCAGCAGT	GCTCAGAGGG	800
	751	CTGGATAAAC	CCATCAAGAA	ACCCAGAAGT	TGGTGGCAGC	AGCATTACAG	800
	751	GTGGATATAT	CACACAAAA	TTCCAGAGGT	TGGTGAGAAC	AGATGGCAGA	800
<div> <div>Exon 5</div> <div>Exon 6</div> </div>							
PGTCD	801	GCTGGTGG--	-TTTCCGAGC	TGGTTTAAAC	ATGGGACTCA	CAGTTACCAC	850
	801	AGGCTGGTG	GCTTCCGAGA	TGGTTTAAAC	ATG-----	--GTTACCAT	850
	801	AGGACTGGTG	GTTCCCAAGC	TGGTTTAAAA	ATGGGACCCA	CAGTTATCAA	850
<div> <div>Exon 6</div> <div>Exon 7</div> </div>							
PGTCD	851	GAAAGAAGAG	ACGCTATAGG	CAACGAAAAG	GAACAAAGAA	AAGAAGACAA	900
	851	GAAAGAAGATG	GAGACATAAA	CGAAGAAAAG	GAACAAAGAA	ACGAAGACGA	900
	851	GAAAGACAACG	TAGAAGGACG	GAGAGAAAAG	GGTAGAAATG	GAGATCGCAT	900
<div> <div>Exon 7</div> <div>Exon 8</div> </div>							
PGTCD	901	CAGAGGAGAG	CTTCCGCTAG	TGGACTGGTT	TAATCCTGAG	AAACGCCCG	950
	901	---AAGCAAG	CTTAAGCTAT	CGGACTGGTT	CAACCCATTT	AAACGCCCG	950
	901	---TGAAGAG	CCTCAGCTAT	GGGACTGGTT	CAATCCAAAG	AACCGCCCG	950
PGTCD	951	AGGTCGTGAC	CATAACCAGA	TGGAAGGCTC	CAGTGGTATG	GGAAGGCACT	1000
	951	AGGTTGTGAC	CATGACGAAG	TGGAAGGCTC	CAGTGGTGTG	GGAAGGCACT	1000
	951	ATGTTTGTGAC	AGTGACCCCG	TGGAAGGCGC	CGATTGTGTG	GGAAGGCACT	1000
PGTCD	1001	TACAACAGAG	CCGCTTTAGA	TAATTATTAT	GCCAAACAGA	AAATTACCGT	1050
	1001	TACAACAGAG	CCGCTTTAGA	CAATTATTAT	GCCAAAGCAGA	AAATTACCGT	1050
	1001	TATGACACAG	CTCTGCTGGA	AAAGTACTAC	GCCACACAGA	AACTCACTGT	1050

FIG. 4C



Exon 8 ← | → Exon 9

PGTCD	1051	GGGCTTGACG	GTTTTTGCTG	TCGGAAGATA	CATTGAGCAT	TACTTGGAGG	1100
BOVGSTA	1051	CGCCTTGACG	GTTTTGCGCG	TCGGAAGATA	CATTGAGCAT	TACTTGGAGG	1100
MUSGLYTNS	1051	GGGCTTGACA	GTGTTTGCTG	TGGGAAAGTA	CATTGAGCAT	TACTTAGAAG	1100
PGTCD	1101	AGTTCTTAAT	ATCTGCAAAT	ACATACITCA	TGGTTGGCCA	CAAAAGTCATC	1150
BOVGSTA	1101	AGTTCTTAAC	GTCTGCTAAT	AAGCACITCA	TGGTTGGCCA	CCAGTCATC	1150
MUSGLYTNS	1101	ACTTCTCTGA	GTCTGCTGAC	ATGTACITCA	TGGTTGGCCA	TCGGGTCTATA	1150
PGTCD	1151	TTTTACATCA	TGGTGGATGA	TATCTCCAGG	ATGCCITTTGA	TAGAGCTGGG	1200
BOVGSTA	1151	TTTTATATCA	TGGTAGATGA	TGTCTCCAGG	ATGCCITTTGA	TAGAGTTGGG	1200
MUSGLYTNS	1151	TTTTACGTCA	TGATAGATGA	CACCTCCCGG	ATGCTCTGTCG	TGCACCTGAA	1200
PGTCD	1201	TCCTCTGCGT	TCCTTTAAAG	TGTTTGAGAT	CAAGTCCGAG	AAGAGGTGGC	1250
BOVGSTA	1201	TCCTCTGCGC	TCCTTTCAAAG	TGTTTAAAGAT	CAAGCCTGAG	AAGAGGTGGC	1250
MUSGLYTNS	1201	CCCTCTACAT	TCCTTACAAG	TCTTTGAGAT	CAGGTCTGAG	AAGAGGTGGC	1250
PGTCD	1251	AAGACATCAG	CATGATGCGC	ATGAAGACCA	TCGGGGAGCA	CATCCTGGCC	1300
BOVGSTA	1251	AGGACATCAG	CATGATGCGC	ATGAAGACTA	TCGGGGAGCA	CATTGTGGCC	1300
MUSGLYTNS	1251	AGGATATCAG	CATGATGCGC	ATGAAGACCA	TTGGGGAGCA	CATCCTGGCC	1300
PGTCD	1301	CACATCCAGC	ACGAGGTGGA	CTTCCTCTTC	TGCATGGACG	TGGATCAGGT	1350
BOVGSTA	1301	CACATCCAGC	ATGAGGTGGA	CTTCCTTTTC	TGCATGGATG	TGGACCAAGT	1350
MUSGLYTNS	1301	CACATCCAGC	ACGAGGTGGA	CTTCCTCTTC	TGCATGGACG	TGGATCAAGT	1350
PGTCD	1351	CTTCCAAAAC	AACCTTTGGG	TGGAGACCCT	GGGCCAGTCG	GTGGCTCAGC	1400
BOVGSTA	1351	CTTCCAAGAC	AAGTTTGGG	TGGAGACCCT	GGGCGAGTCG	GTGGCCACAGC	1400
MUSGLYTNS	1351	CTTCCAAGAC	AACCTTCGGG	TGGAAACTCT	GGGCCAGCTG	GTAGCACACAGC	1400

FIG. 4D

PGTCD	1401	TACAGGCCTG	GTGGTACAAG	GCACATCCTG	ACGAGTTCAC	CTACGAGAGG	1450
BOVGSTA	1401	TACAAGCCTG	GTGGTACAAG	GCAGATCCCA	ATGACTTCAC	CTACGAGAGG	1450
MUSGLYTNS	1401	TCCAGGCCTG	GTGGTACAAG	GCCAGTCCCG	AGAAGTTCAC	CTATGAGAGG	1450
PGTCD	1451	CGGAAGGAGT	CCGCAGCCTA	CATTCCGTTT	GGCCAGGGGG	ATTTTATTATA	1500
BOVGSTA	1451	CGGAAGGAGT	CTGCAGCATA	CATTCCCTTC	GGCGAAGGGG	ATTTTATTATA	1500
MUSGLYTNS	1451	CGGGAACGTG	CGGCCGCGTA	CATTCCATTTC	GGAGAGGGGG	ATTTTACTATA	1500
PGTCD	1501	CCACGCAGCC	ATTTTGTGGG	GAACACCCAC	TCAGGTTCCTA	AACATCACTC	1550
BOVGSTA	1501	CCATGCAGCC	ATTTTGTGGG	GAACACCCAC	TCAGGTTCCTT	AACATCACCC	1550
MUSGLYTNS	1501	CCACGGGGCC	ATTTTGTGGG	GAACGGCTAC	TCACATTCTC	AACCTCACCA	1550
PGTCD	1551	AGGAGTGCTT	CAAGGGAATC	CTCCAGGACA	AGGAAAATGA	CATAGAAGCC	1600
BOVGSTA	1551	AGGAATGCTT	CAAGGGAATC	CTCAAGGACA	AGAAAATGA	CATAGAAGCC	1600
MUSGLYTNS	1551	GGGAGTGCTT	TAAGGGGATC	CTCCAGGACA	AGAAACATGA	CATAGAAGCC	1600
PGTCD	1601	GAGTGGCATG	ATGAAAGCCA	TCTAAACAAG	TATTTCCCTTC	TCAACAAAACC	1650
BOVGSTA	1601	CAATGGCATG	ATGAAAGCCA	TCTAAACAAG	TATTTCCCTTC	TCAACAAAACC	1650
MUSGLYTNS	1601	CAGTGGCATG	ATGAGAGCCA	CCTCAACAAA	TACTTCCTTT	TCAACAAAACC	1650
PGTCD	1651	CACTAAAATC	TTATCCCCCAG	AATACTGCTG	GGATTATCAT	ATAGGCATGT	1700
BOVGSTA	1651	TACTAAAATC	TTATCCCCCAG	AATACTGCTG	GGATTATCAT	ATAGGCCTAC	1700
MUSGLYTNS	1651	CACTAAAATC	CTATCTCCAG	AGTATTGCTG	GGACTATCAG	ATAGGCCTGC	1700
PGTCD	1701	CTGTGGATAT	TAGGATTGTC	AAGATAGCTT	GGCAGAAAAA	AGAGTATAAT	1750
BOVGSTA	1701	CTGCGGATAT	TAAAGTTGTC	AAGATGTCTT	GGCAGACAAA	AGAGTATAAT	1750
MUSGLYTNS	1701	CTTCAGATAT	TAAAAGTGTG	AAGGTAGCTT	GGCAGACAAA	AGAGTATAAT	1750

FIG.4E

PGTCD	1751	TTGGTTAGAA	ATAACATCTG	ACTTTAAATT	GTGCCAGCAG	TTTTCTGAAT	1800
BOVGSTA	1751	GTGGTTAGAA	ATAATGTCTG	ACTT-----T	GTGCCAGTAC	ATTTCTGAAT	1800
MUSGLYTNS	1751	TTGGTTAGAA	ATAATGTCTG	ACTTCAAAAT	GTG-----	--ATGGAAAC	1800
				Stop			
PGTCD	1801	TTGAAAGAGT	ATTACTCTGG	CTACTTCCTC	AGAGAAGTAG	---CACTTAA	1850
BOVGSTA	1801	TTGAGAGAGT	ATTATTCTGG	CTACTTCCTC	AGAAAAGTAA	---CACTTAA	1850
MUSGLYTNS	1801	TTGACAC--T	ATTACTCTGG	CTAATTCCTC	AAACAAGTAG	CAACACTTGA	1850
PGTCD	1851	TTTTAACTTT	TAAAAAAATA	CTAACAAAA-	----TACCAA	CACAGTAA-G	1900
BOVGSTA	1851	TTTTAACTTA	AAAAAAATA	CTAACAAAA-	----GACCAA	CACAGCAA-A	1900
MUSGLYTNS	1851	TTTCAACTTT	TAAAGAA-A	CAATCAAAAC	CAAAACCCAC	TACCATGGCA	1900
PGTCD	1901	TACATATTAT	TCTTCCTTGC	AACTTTGAGC	CTTGTCAAAT	GGGAGAAATGA	1950
BOVGSTA	1901	TACATATTAT	TCTTCCTTGT	AACTTTGAGC	CTTGTAAATAC	GGGAGAAATGA	1950
MUSGLYTNS	1901	AACAGATGAT	TTCTCCT-GA	CACCTTGAGC	CT-GTAATAT	GTGAGAAAGA	1950
PGTCD	1951	CTCTGTGG--	--TAATCAGA	TGTAAATTCC	CAGTGATTTC	2000
BOVGSTA	1951	ACCTGTGG--	--TAATCAGA	TGTAAATTCC	CAGTGATTTC	TTACCTATTT	2000
MUSGLYTNS	1951	GTCATATGGCA	AGTAATCAGG	TATAAATTCT	CAATGATTTC	TTATATATTC	2000
PGTCD	2001	2050
BOVGSTA	2001	TTGGTTGTGG	GGCGGGGAA	TGGATACACC	ATCAGTTGAA	CC.....	2050
MUSGLYTNS	2001	TGGGTCCTGG	GAAAACTTGA	TTCTAGAAAT	CAAAATTAAAT	TTGACAAAGG	2050
PGTCD	2051	2100
BOVGSTA	2051	2100
MUSGLYTNS	2051	AAAAGCAGAT	GCCGGAAACT	TCTTCCCAGT	CTGTCAATACA	ATTCACCACT	2100

FIG. 4F

[illegible]

FIG. 4G

PGTCD	2451
BOVGSTA	2451
MUSGLYTNS	2451	GTTACAAACA	CAGACAGCTT	TCTTCAGGAT	GAATAACACG	AGGAATTGAA	AGGAATTGAA	AGGAATTGAA	AGGAATTGAA	AGGAATTGAA	AGGAATTGAA
PGTCD	2501
BOVGSTA	2501
MUSGLYTNS	2501	TGGAAAGTGT	GTTCAATTTG	TTTTGCCCAA	ATTGTATTCA	TGCTGTTAGC	TGCTGTTAGC	TGCTGTTAGC	TGCTGTTAGC	TGCTGTTAGC	TGCTGTTAGC
PGTCD	2551
BOVGSTA	2551
MUSGLYTNS	2551	TTTGTGTGTT	GAGCCCTGTG	GAGAGGGTGT	GACTGTATCA	GGGAAGGAGA	GGGAAGGAGA	GGGAAGGAGA	GGGAAGGAGA	GGGAAGGAGA	GGGAAGGAGA
PGTCD	2601
BOVGSTA	2601
MUSGLYTNS	2601	GTACCCTCAC	GGACTGAGGA	CCAGCACCCCT	ATTATATCAG	AAGACAATCT	AAGACAATCT	AAGACAATCT	AAGACAATCT	AAGACAATCT	AAGACAATCT
PGTCD	2651
BOVGSTA	2651
MUSGLYTNS	2651	CTCATCATCA	GGTCCCTACCT	ACAACCTGCT	CTGAACCTCC	GAGTTCCTCA	GAGTTCCTCA	GAGTTCCTCA	GAGTTCCTCA	GAGTTCCTCA	GAGTTCCTCA
PGTCD	2701
BOVGSTA	2701
MUSGLYTNS	2701	GCCCATCGTG	TTCCAGTGTG	GGGGCCCTGTA	TGGAGCAGGT	GACTGAAGAC	GACTGAAGAC	GACTGAAGAC	GACTGAAGAC	GACTGAAGAC	GACTGAAGAC
PGTCD	2751
BOVGSTA	2751
MUSGLYTNS	2751	AAAGCCCCCT	GTCACATGAC	CTCATTTCCC	CTGCTCTAGT	ACTATGCAAG	ACTATGCAAG	ACTATGCAAG	ACTATGCAAG	ACTATGCAAG	ACTATGCAAG

FIG. 4H

FIG. 41

		Ex4 ▼	Ex5	Ex5 ▼	Ex6	
PGT[Frame 1]	1	MNVKGRVLS	MLLVSTVMVV	FWEYINSPEG	SLFWIYQSKN	PEVG-SSAQR 50
BGT[Frame 1]	1	MNVKGVILS	MLVVSTVIVV	FWEYIHSPEG	SLFWINPSRN	PEVGGSSIQK 50
MGT[Frame 1]	1	MNVKGVILL	MLIVSTVVVV	FWEYVNSPDG	SFLWIYHTKI	PEVGENRWQK 50

		Ex6 ▼	Ex7	Ex7 ▼	Ex8	
PGT[Frame 1]	51	GWWFPSWFNN	GTHSYHEEED	AIGNEKEQRK	EDNRGELPLV	DWFNPEKRPE 100
BGT[Frame 1]	51	GWWLPRWFNN	G---YHEEDG	DINEEKEQRN	ED-ESKLKLS	DWFNPFKRPE 100
MGT[Frame 1]	51	DWWFPSWFKN	GTHSYQEDNV	EGRREK-GRN	GDRIEEPQLW	DWFNPKNRPD 100

				Ex8 ▼	Ex9	
PGT[Frame 1]	101	VVTITRWKAP	VWEGTYNRA	VLDNYNKQK	ITVGLTVFAV	GRYIEHYLEE 150
BGT[Frame 1]	101	VVTMTKWKAP	VWEGTYNRA	VLDNYYAKQK	ITVGLTVFAV	GRYIEHYLEE 150
MGT[Frame 1]	101	VLTVTPWKAP	IVWEGTYDTA	LLEKYYATQK	LTVGLTVFAV	GKYIEHYLED 150

PGT[Frame 1]	151	FLISANTYFM	VGHKVIFYIM	VDDISRMPLI	ELGPLRSFKV	FEIKSEKRWQ 200
BGT[Frame 1]	151	FLTSANKHFM	VGHPVIFYIM	VDDVSRMPLI	ELGPLRSFKV	FKIKPEKRWQ 200
MGT[Frame 1]	151	FLESADMYFM	VGHRVIFYVM	IDDTSRMPVV	HLNPLHSLQV	FEIRSEKRWQ 200

FIG. 5A

PGT[Frame 1]201	DISMMRMKTI	GEHILAHIQH	EVDFLCMDV	DQVFQNNFGV	ETLGQSVAQL	250
BGT[Frame 1]201	DISMMRMKTI	GEHIVAHIQH	EVDFLCMDV	DQVFQDKFGV	ETLGESVAQL	250
MGT[Frame 1]201	DISMMRMKTI	GEHILAHIQH	EVDFLCMDV	DQVFQDNFGV	ETLGQLVAQL	250
PGT[Frame 1]251	QAWWYKAHPD	EFTYERRKES	AAVIPFGQGD	FYYHAAIFGG	TPTQVLNITQ	300
BGT[Frame 1]251	QAWWYKADPN	DFTYERRKES	AAVIPFGEGD	FYYHAAIFGG	TPTQVLNITQ	300
MGT[Frame 1]251	QAWWYKASPE	KFTYERRELS	AAVIPFGEGD	FYYHAAIFGG	TPTHILNLTR	300
PGT[Frame 1]301	ECFKGILQDK	ENDIEAEWHD	ESHLNKYFLL	NKPTKILSPE	YCWYDHIGMS	350
BGT[Frame 1]301	ECFKGILKDK	KNDIEAQWHD	ESHLNKYFLL	NKPTKILSPE	YCWYDHIGLP	350
MGT[Frame 1]301	ECFKGILQDK	KHDIEAQWHD	ESHLNKYFLF	NKPTKILSPE	YCWYQIGLP	350
PGT[Frame 1]351	VDIKIVKIAW	QKKEYNLVRN	NI*	400
BGT[Frame 1]351	ADIKLVKMSW	QTKEYNVVRN	NV*	400
MGT[Frame 1]351	SDIKSVKVAW	QTKEYNLVRN	NV*	400

FIG. 5B

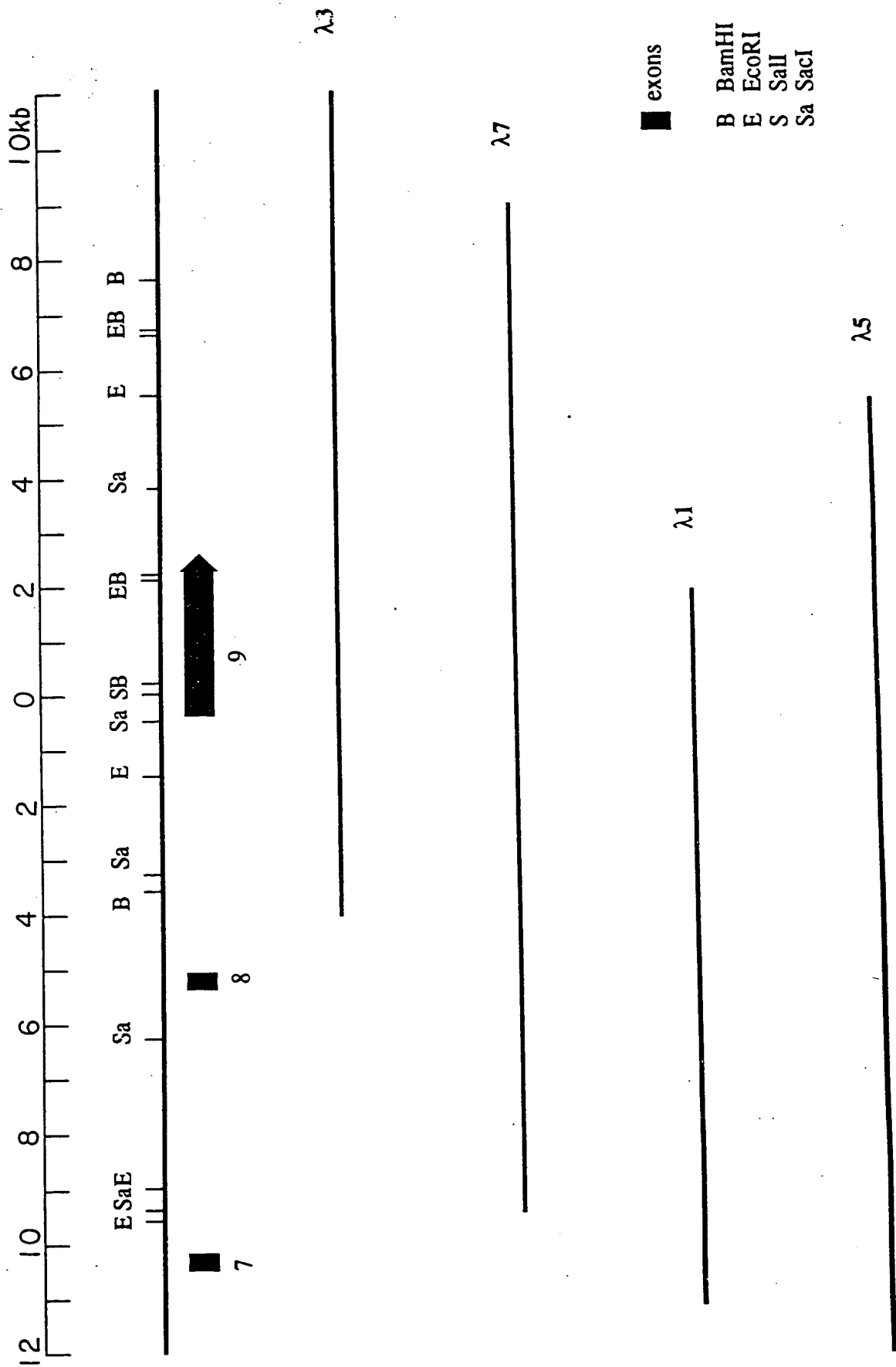
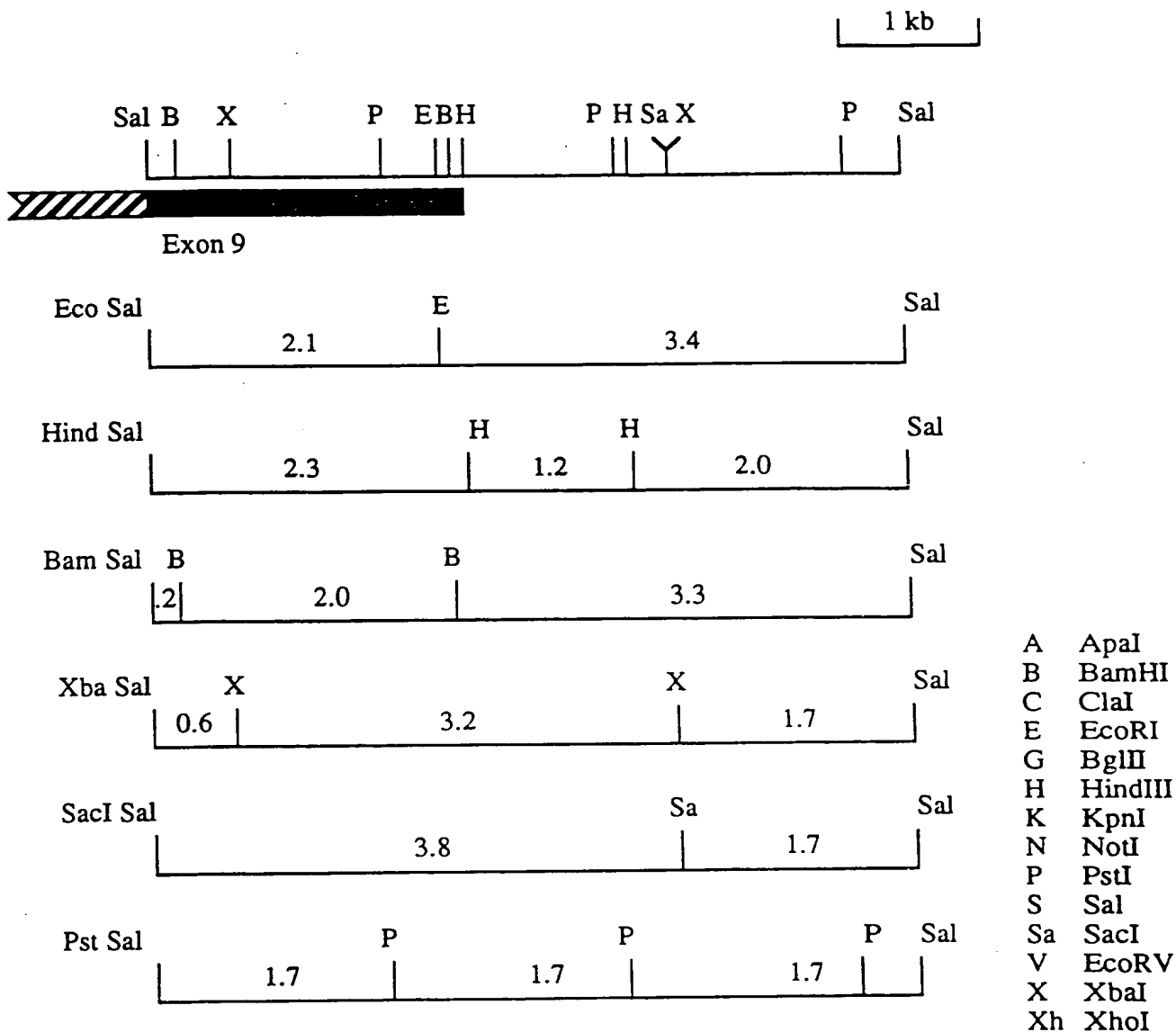


FIG. 6

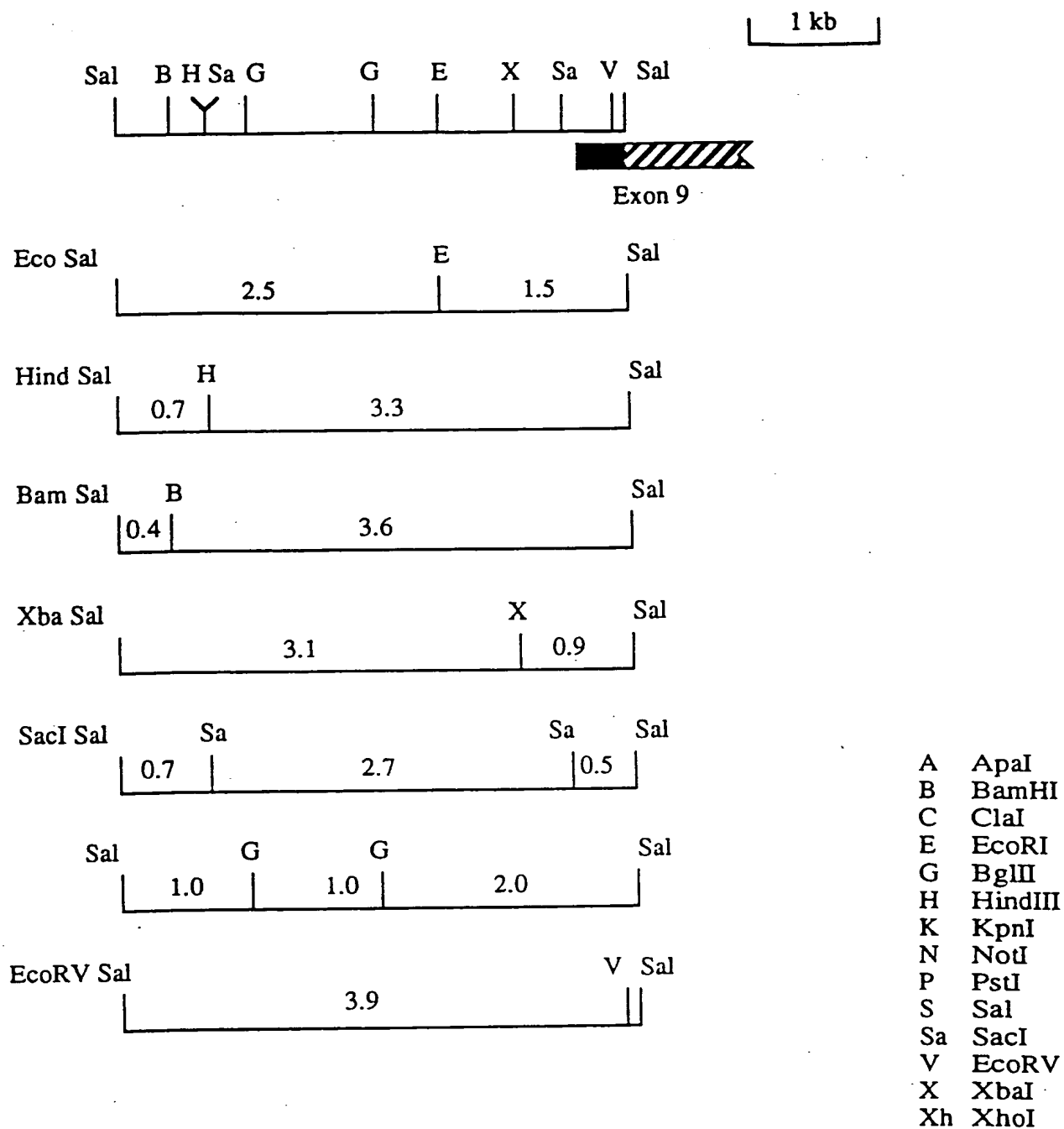


No sites for: BglII, Nde, PvuI, Xho, Kpn, SacII, EcoRV, Sma, Cla, Apa, Not

pBS+KS: SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn



FIG. 7



No sites for: Nde, PvuI, Xho, Kpn, SacII, Sma, Cla, Apa, Not

Unmapped sites for: Pst, PvuII

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn

FIG. 8

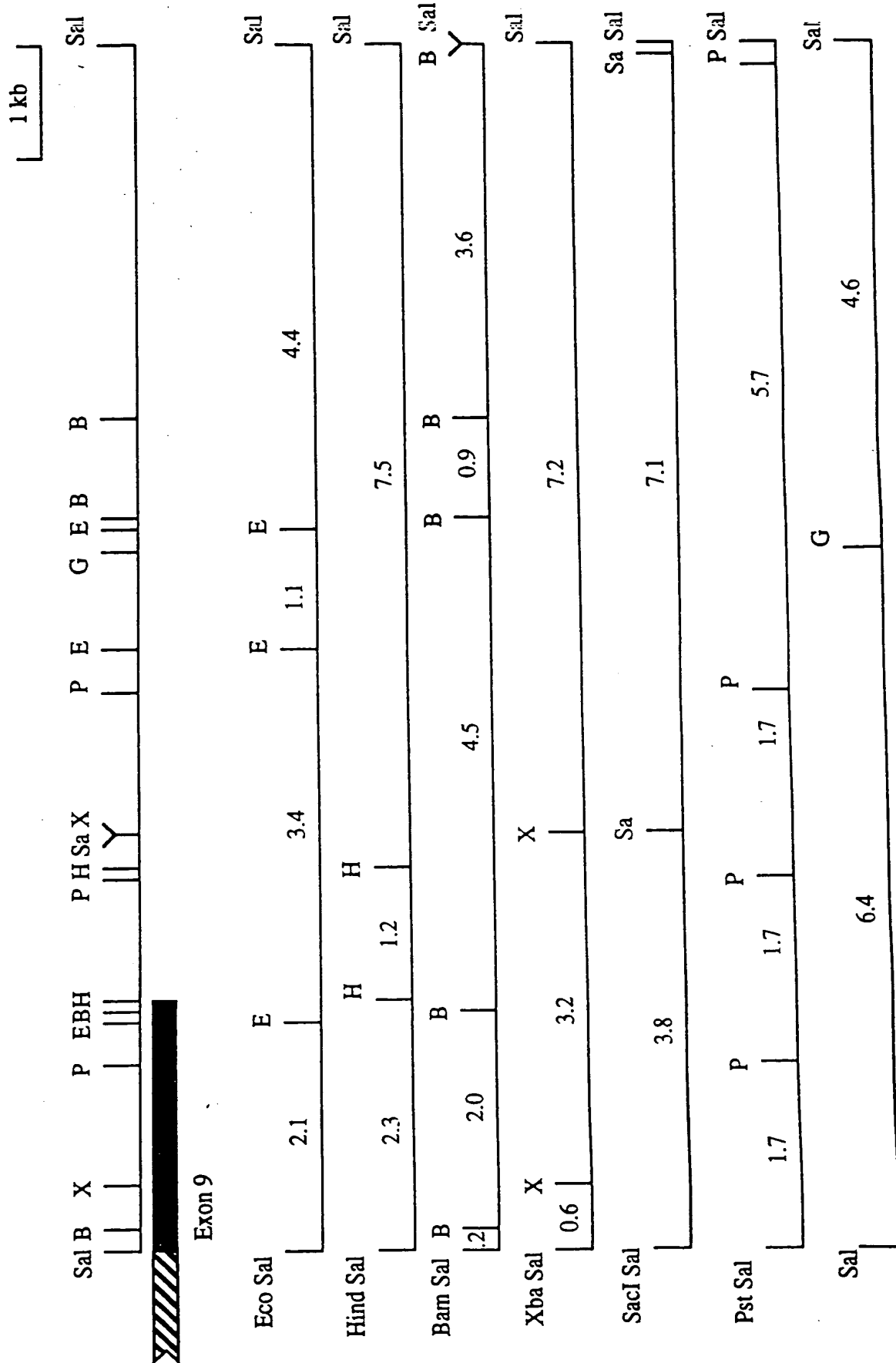


FIG. 9a

A	Apal
B	BamHI
C	ClaI
E	EcoRI
G	BglII
H	HindIII
K	KpnI
N	NotI
P	PstI
S	Sal
Sa	SacI
V	EcoRV
X	XbaI
Xh	XhoI

No sites for: Xho, Kpn, SacII, Sma, Cla, EcoRV, Apa, Not, PvuI, Nde

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn



FIG. 9b

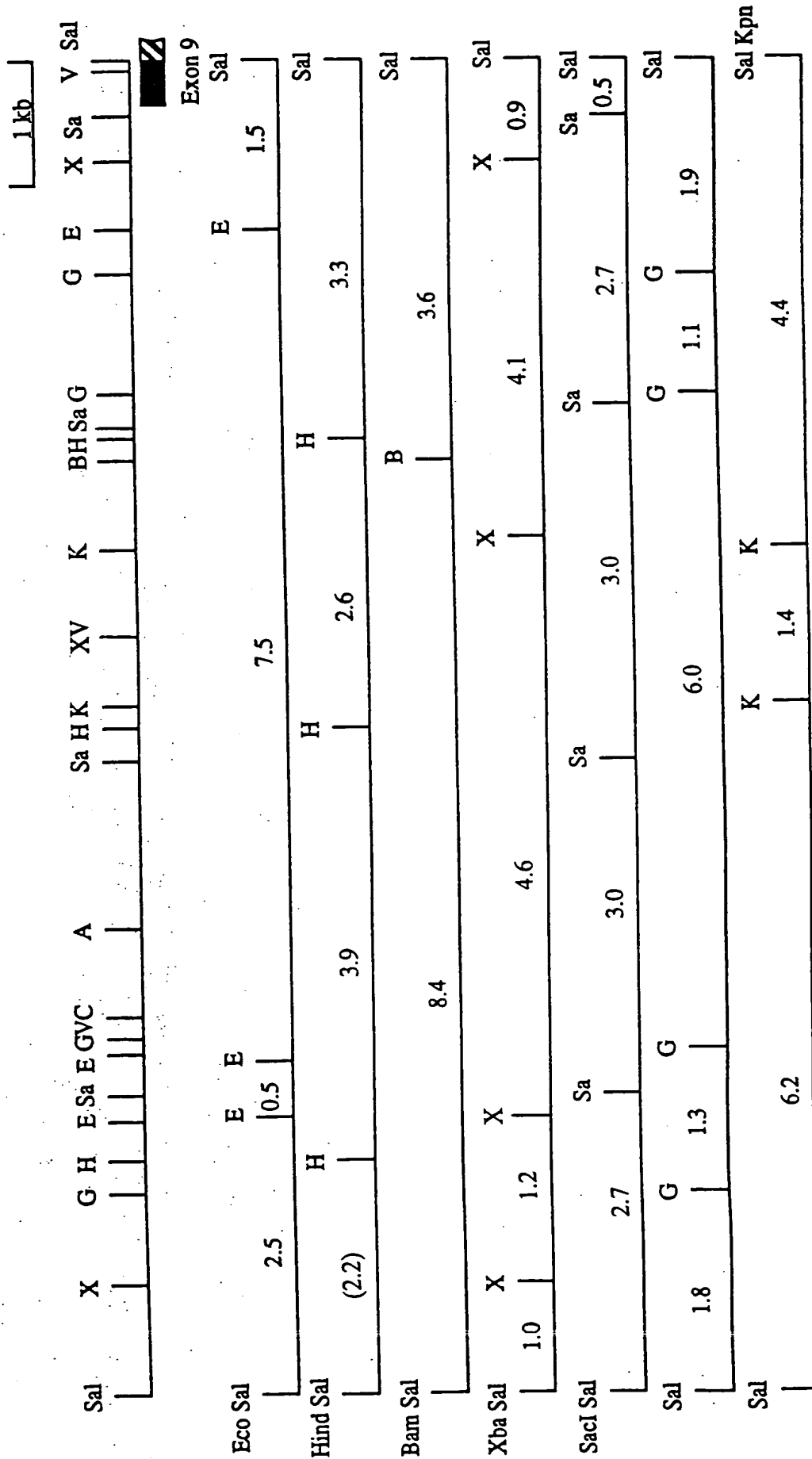


FIG. 10a

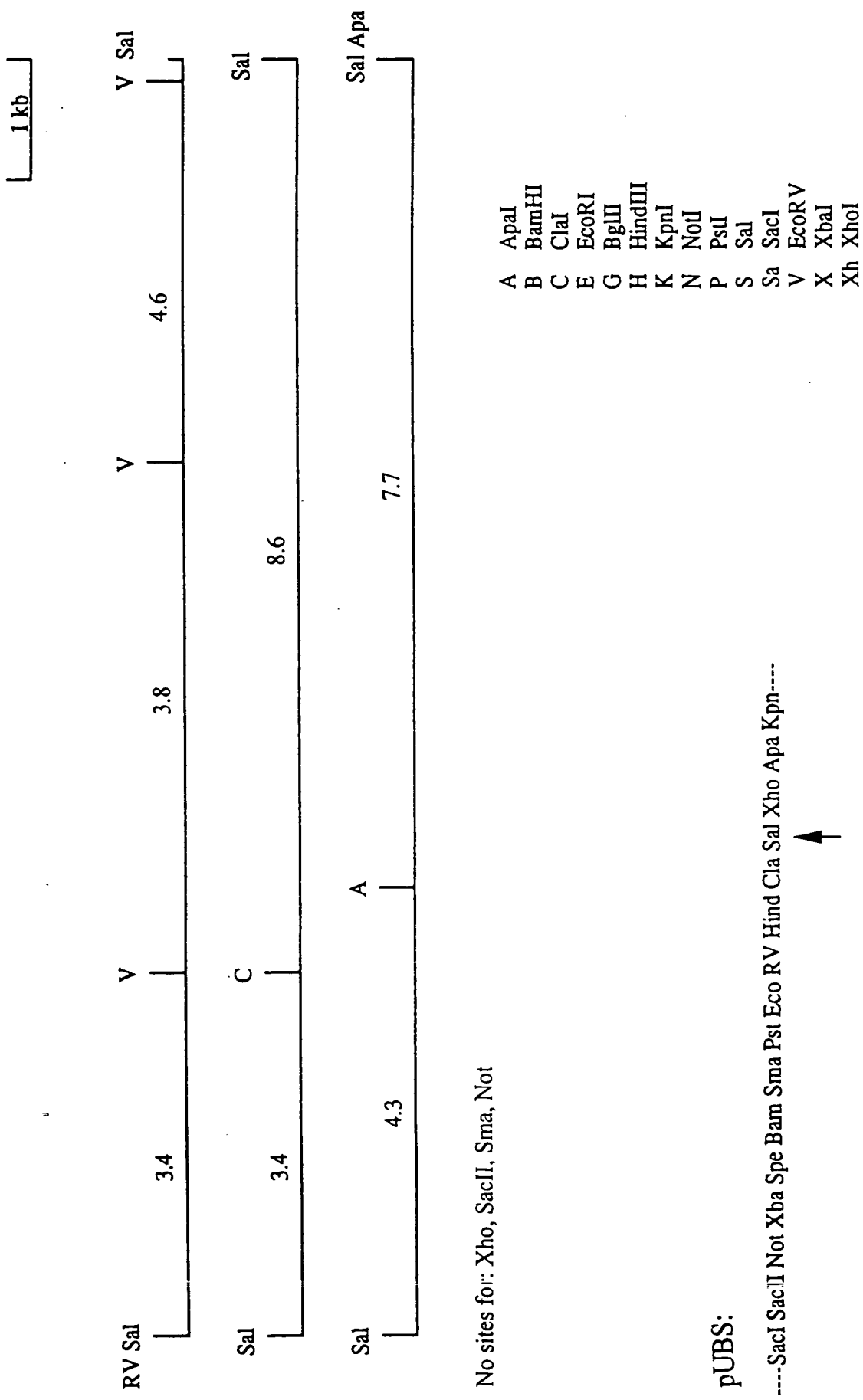


FIG. 10b

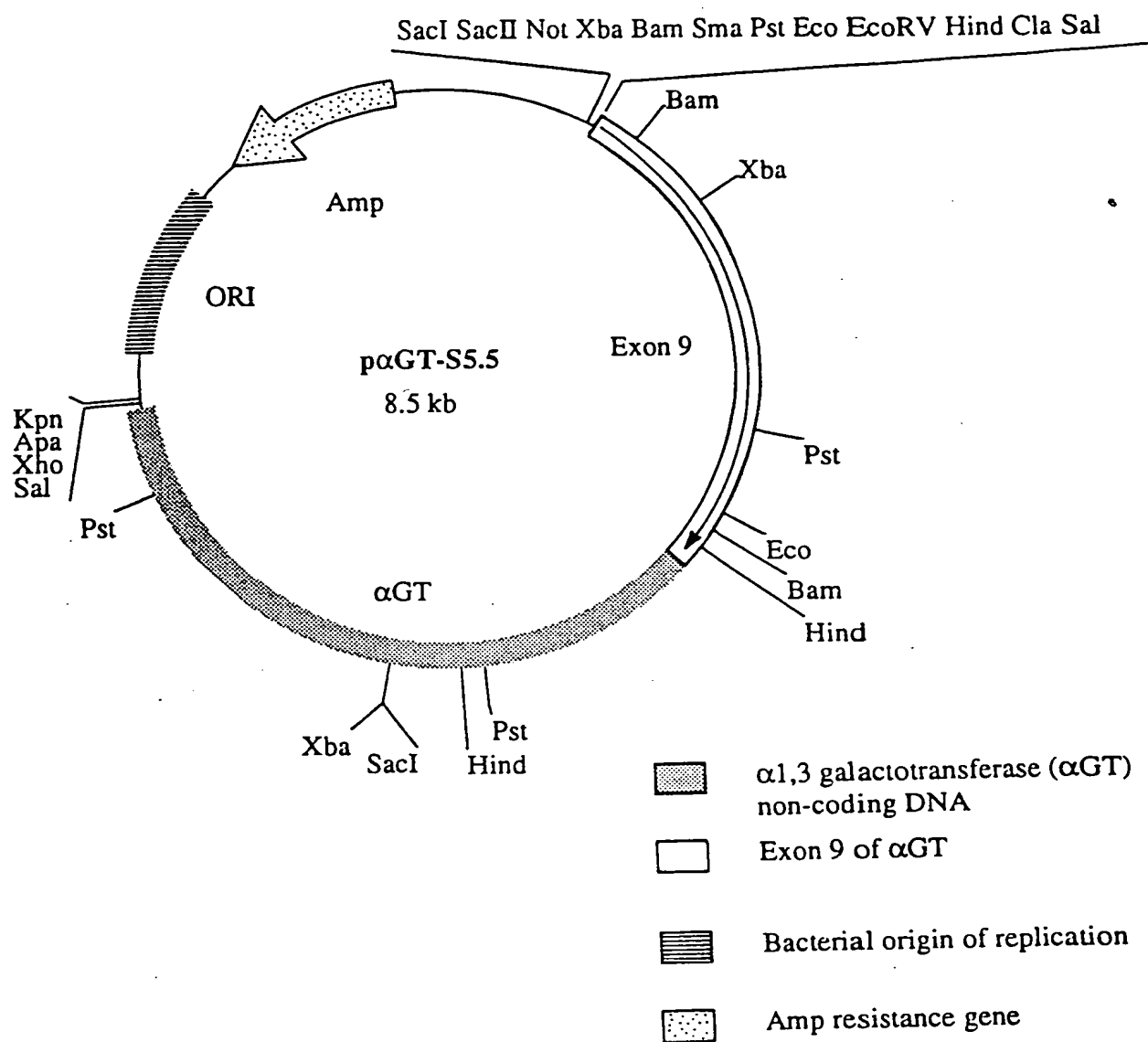


FIG. II

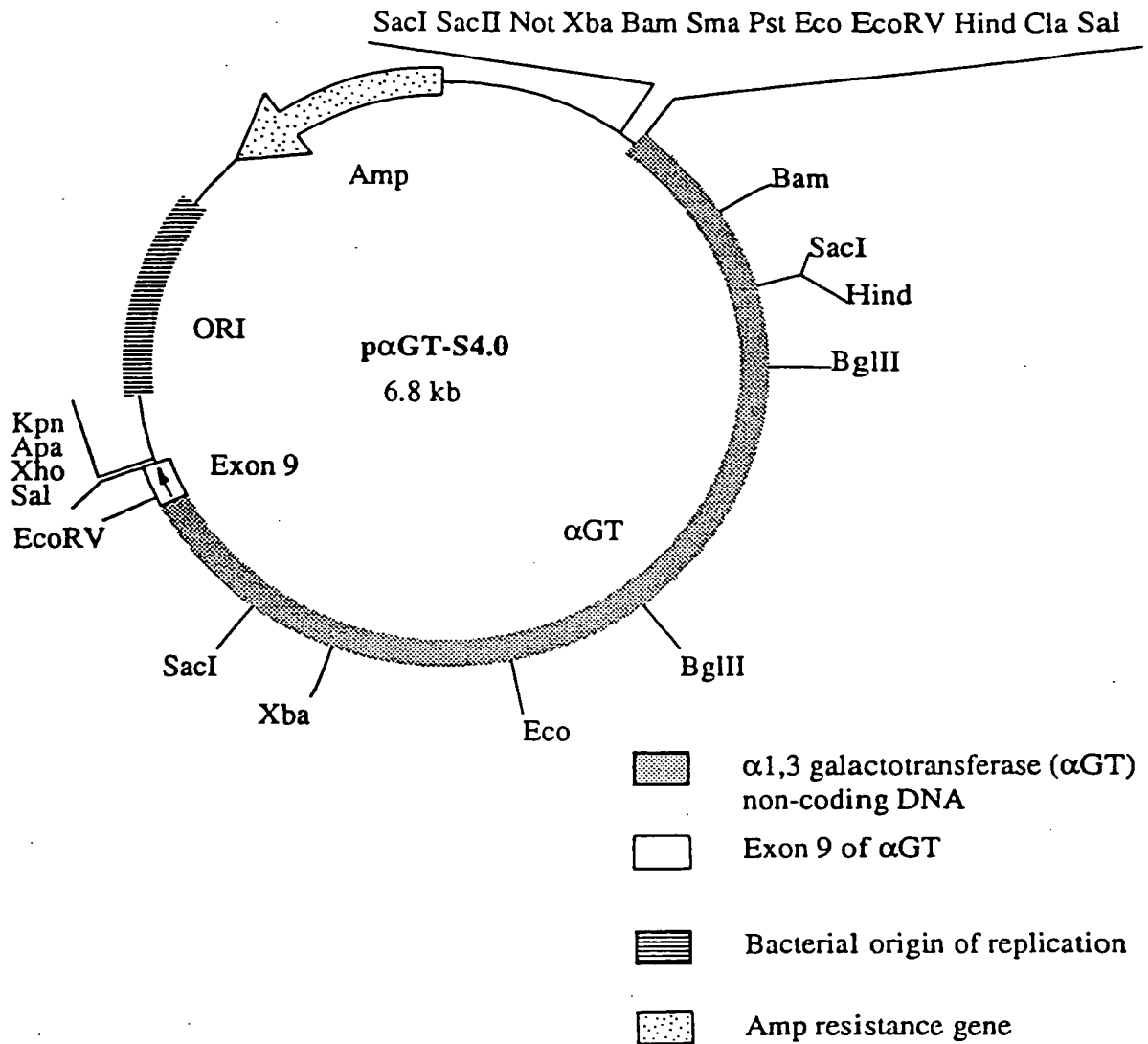
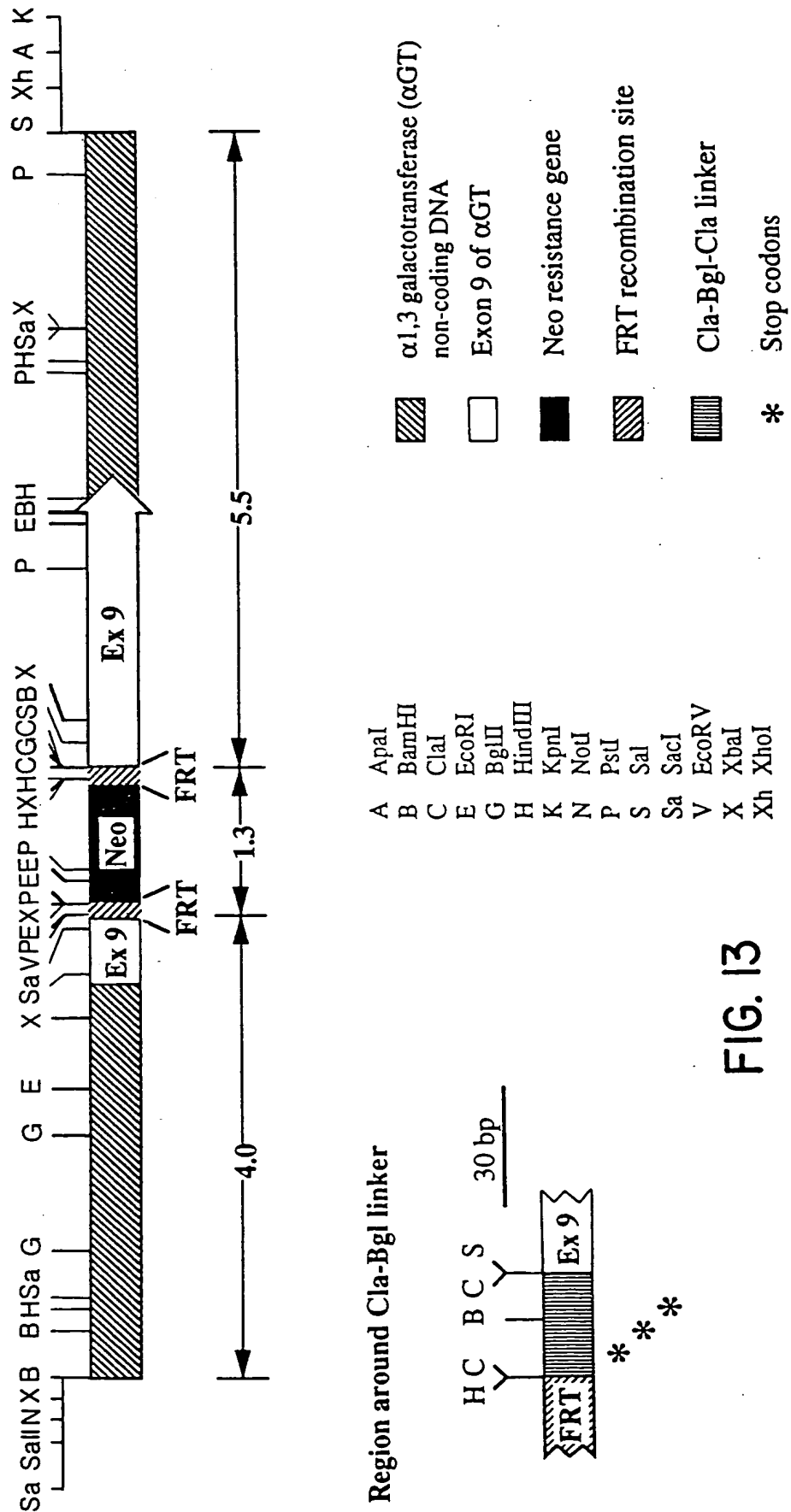


FIG. 12



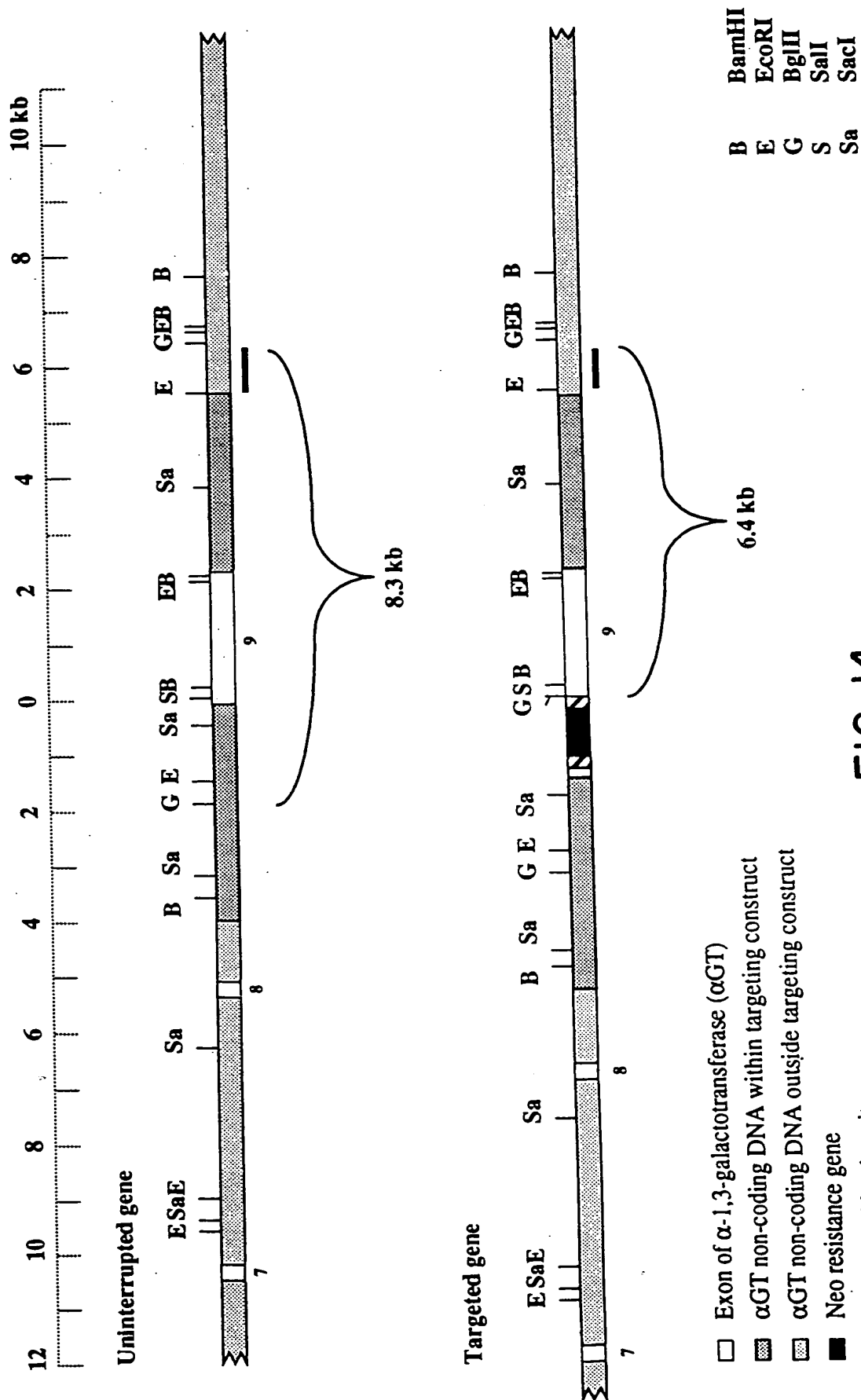


FIG. 14

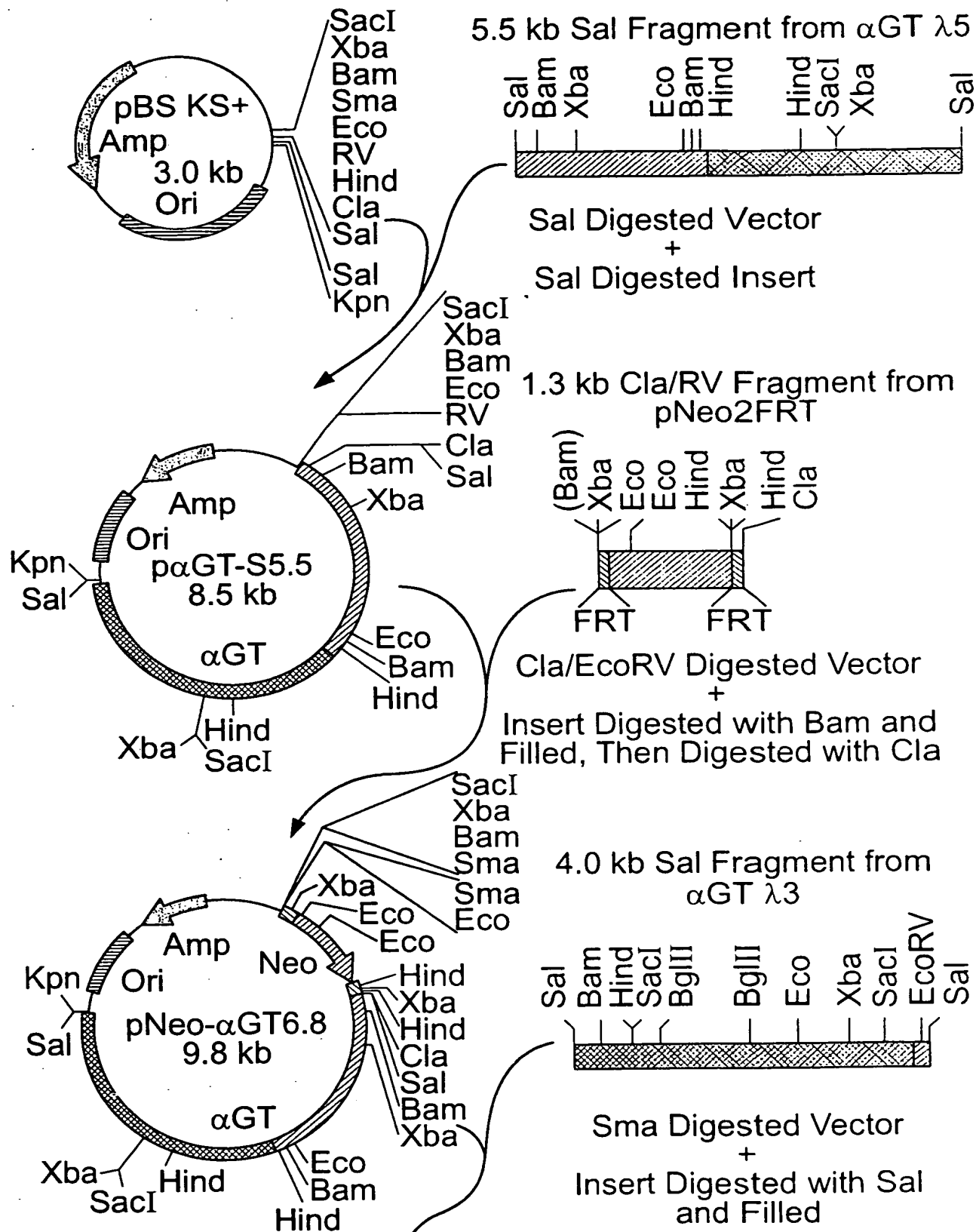


FIG. 15A

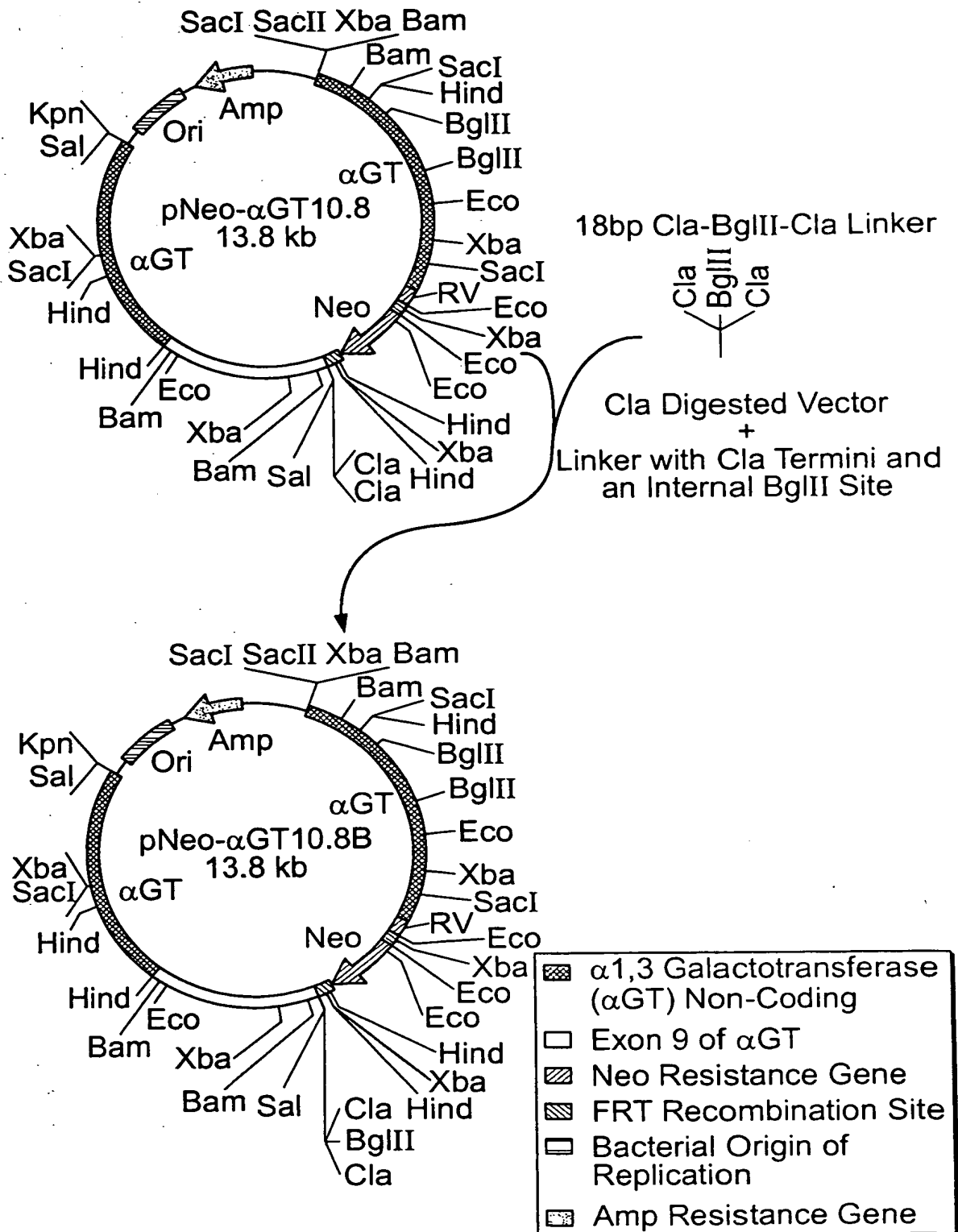


FIG. 15B

```

10      20      30      40      50      60
GAGGGCTGCA GGAATTTCGAT GATCCCCCAG CTTGAAGTTC CTATTCGGAA GTTCCTATTC

70      80      90      100     110     120
TCTAGAAAGT ATAGGAACTT CAAGCTGGGC TGCAGGAATT CGATTGAGC AGTGTGGTTT

130     140     150     160     170     180
TGCAAGAGGA AGCAAAAAGC CTCTCCACCC AGGCCTGGAA TGTTCACC CAATGTCGAG

190     200     210     220     230     240
CAGTGTGGTT TTGCAAGAGG AAGCAAAAAG CCTCTCCACC CAGGCCTGGA ATGTTTCCAC

250     260     270     280     290     300
CCAATGTCGA GCAAACCCCG CCCAGCGTCT TGTCATTGGC GAATTCGAAC ACGCAGATGC

310     320     330     340     350     360
AGTCGGGGCG GCGCGGTCCC AGGTCCACTT GGCATATTAA GGTGACCGT GTGGCCTCGA

370     380     390     400     410     420
ACACCGAGCG ACCCTGCAGC CAATATGGGA TCGGCCATTG AACAGATGG ATTGCACGCA

430     440     450     460     470     480
GGTTCTCCGG CCGCTTGGGT GGAGAGGCTA TTCGGCTATG ACTGGGCACA ACAGACAATC

490     500     510     520     530     540
GGCTGCTCTG ATGCCGCCGT GTTCCGGCTG TCAGCGCAGG GGCGCCCGGT TCTTTTTGTG

550     560     570     580     590     600
AAGACCGACC TGTCCGGTGC CCTGAATGAA CTCCAAGACG AGGCAGCGCG GCTATCGTGG

610     620     630     640     650     660
CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG TTGTCCTGA AGCGGGAAGG

670     680     690     700     710     720
GACTGGCTGC TATTGGGCGA AGTGCCGGGG CAGGATCTCC TGTCTCTCA CCTTGCTCCT

730     740     750     760     770     780
GCCGAGAAAG TATCCATCAT GGCTGATGCA ATGCCGGCGC TGCATACGCT TGATCCGGCT

790     800     810     820     830     840
ACCTGCCCAT TCGACCACCA AGCGAAACAT CGCATCGAGC GAGCACGTAC TCGGATGGAA

850     860     870     880     890     900
GCCGGTCTTG TCGATCAGGA TGATCTGGAC GAAGAGCATC AGGGGCTCGC GCCAGCCGAA

910     920     930     940     950     960
CTGTTGCGCA GGCTCAAGGC GCGGATGCCC GACGGCGAGG ATCTCGTCGT GACCCATGGC

970     980     990     1000    1010    1020
GATGCCTGCT TGCCGAATAT CATGGTGGAA AATGGCCGCT TTTCTGGATT CATCGACTGT

1030    1040    1050    1060    1070    1080
GGCCGGCTGG GTGTGGCGGA CCGCTATCAG GACATAGCGT TGGCTACCCG TGATATTGCT

1090    1100    1110    1120    1130    1140
GAAGAGCTTG GCGGCGAATG GGCTGACCGC TTCTCTGTGC TTTACGGTAT CGCCGCTCCC

```

FIG. 16A

1150	1160	1170	1180	1190	1200
GATTCGCAGC	GCATCGCCTT	CTATCGCCTT	CTTGACGAGT	TCTTCTGAGG	GGATCGGCAA
1210	1220	1230	1240	1250	1260
TAAAAAGACA	GAATAAAACG	CACGGGTGTT	GGGCGTTTGT	TCGGATCATC	AAGCTTGAAG
1270	1280	1290	1300	1310	1320
TTCTTATTCC	GAAGTTCCTA	TTCTCTAGAA	AGTATAGGAA	CTTCAAGCTT	ATCGATGAGT
1330	1340	1350	1360	1370	1380
AGATCTTGAT	CGATACCGTC

Linker sequences : 0-28

FRT : 29-104

Polyoma virus enhancer repeats : 105-249

Herpes Simplex Virus Tyrosine Kinase promoter : 250-385

Neomycin phosphotransferase coding region : 385-1188

Herpes Simplex Virus Tyrosine Kinase PolyA signal : 1189-1249

FRT : 1250-1310

Linker sequences : 1311-1340

FIG. 16B

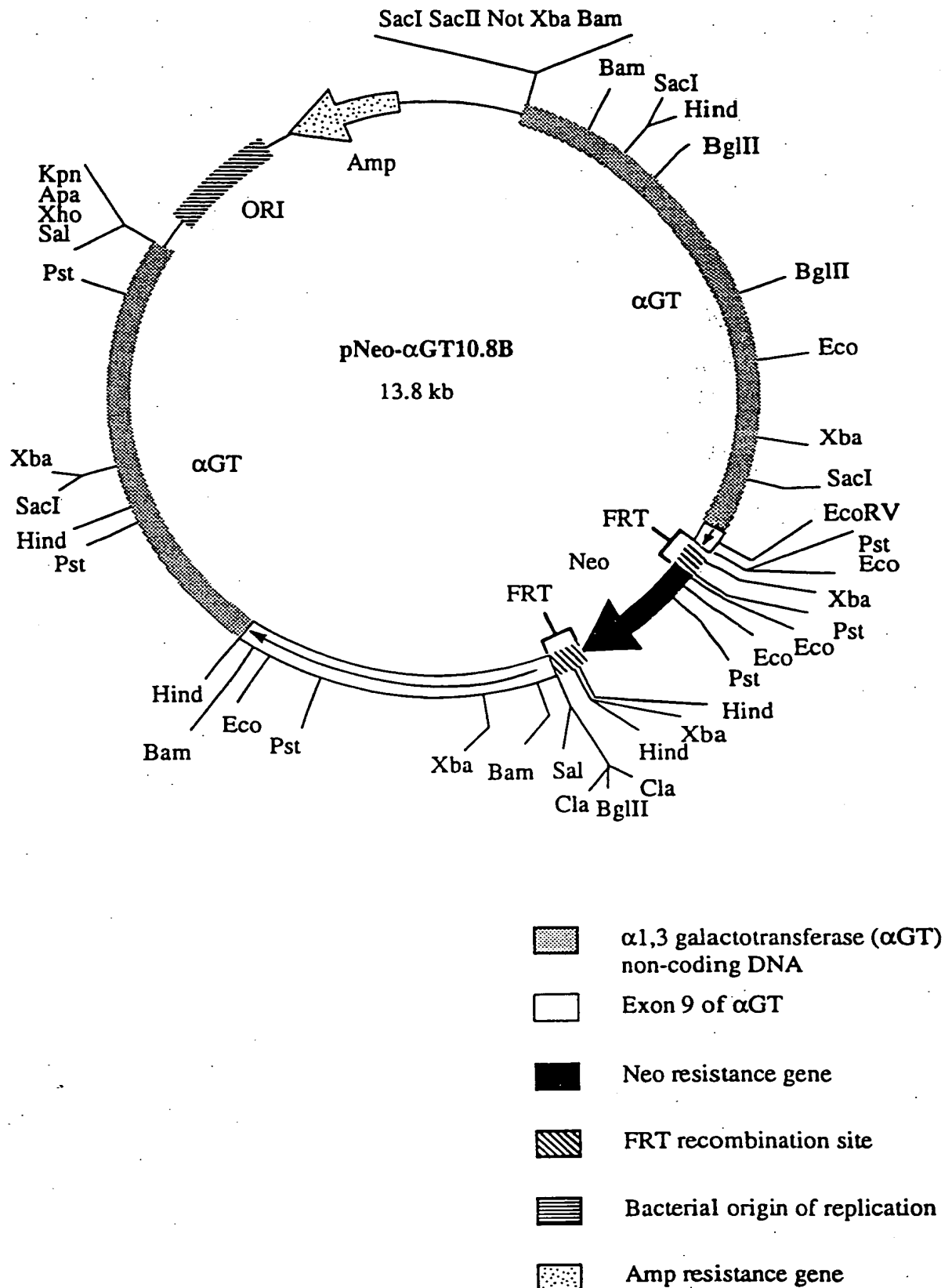


FIG. 17

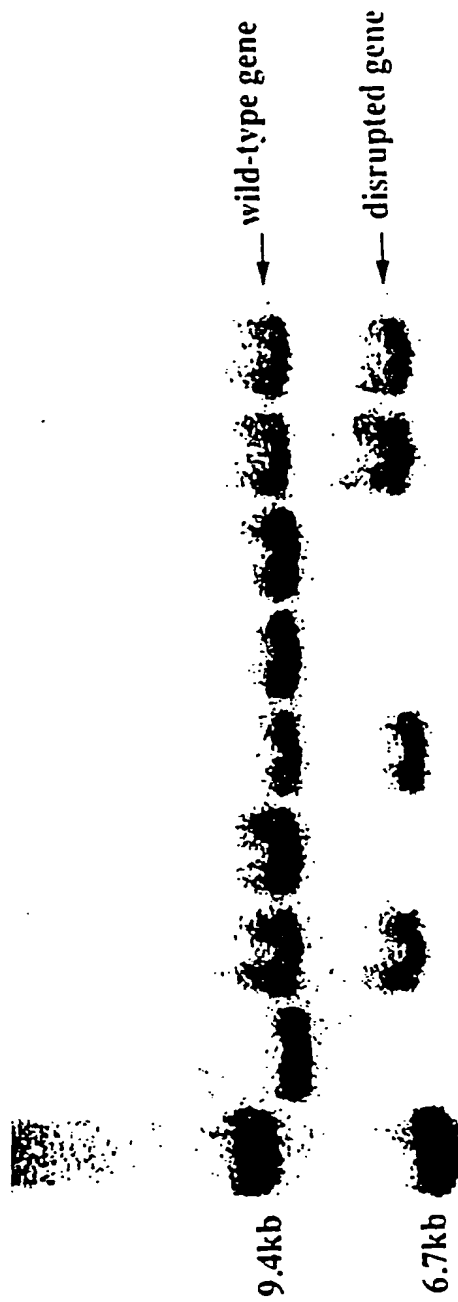


FIG. 18

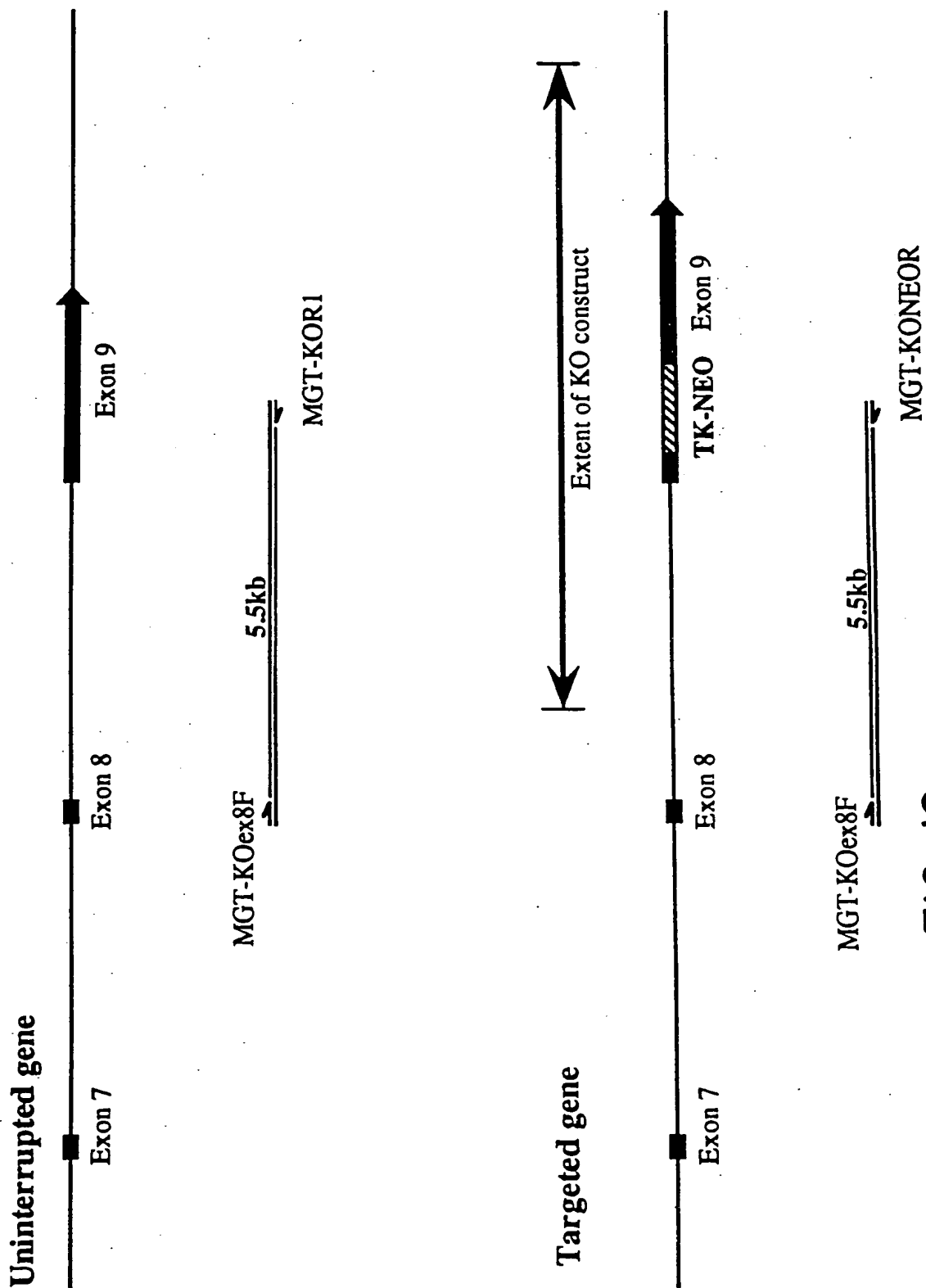
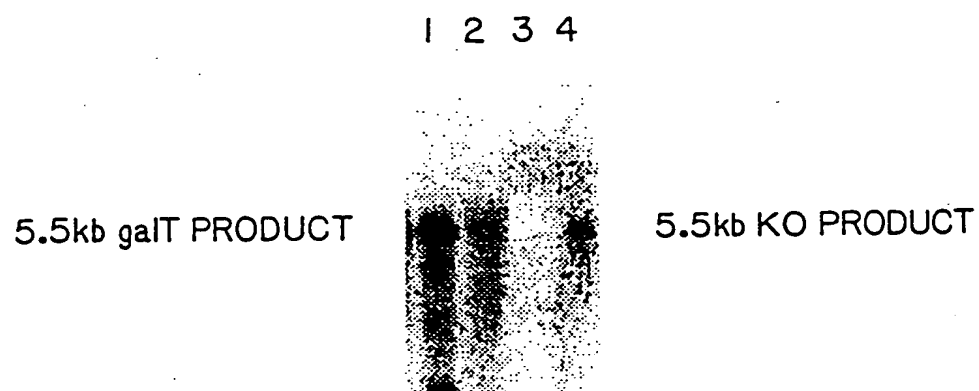


FIG. 19



1. CBAC TEMPLATE; WILD TYPE PRIMERS
2. 7C2 TEMPLATE; WILD TYPE PRIMERS
3. CBAC TEMPLATE; KO PRIMERS
4. 7C2 TEMPLATE; KO PRIMERS

FIG. 20

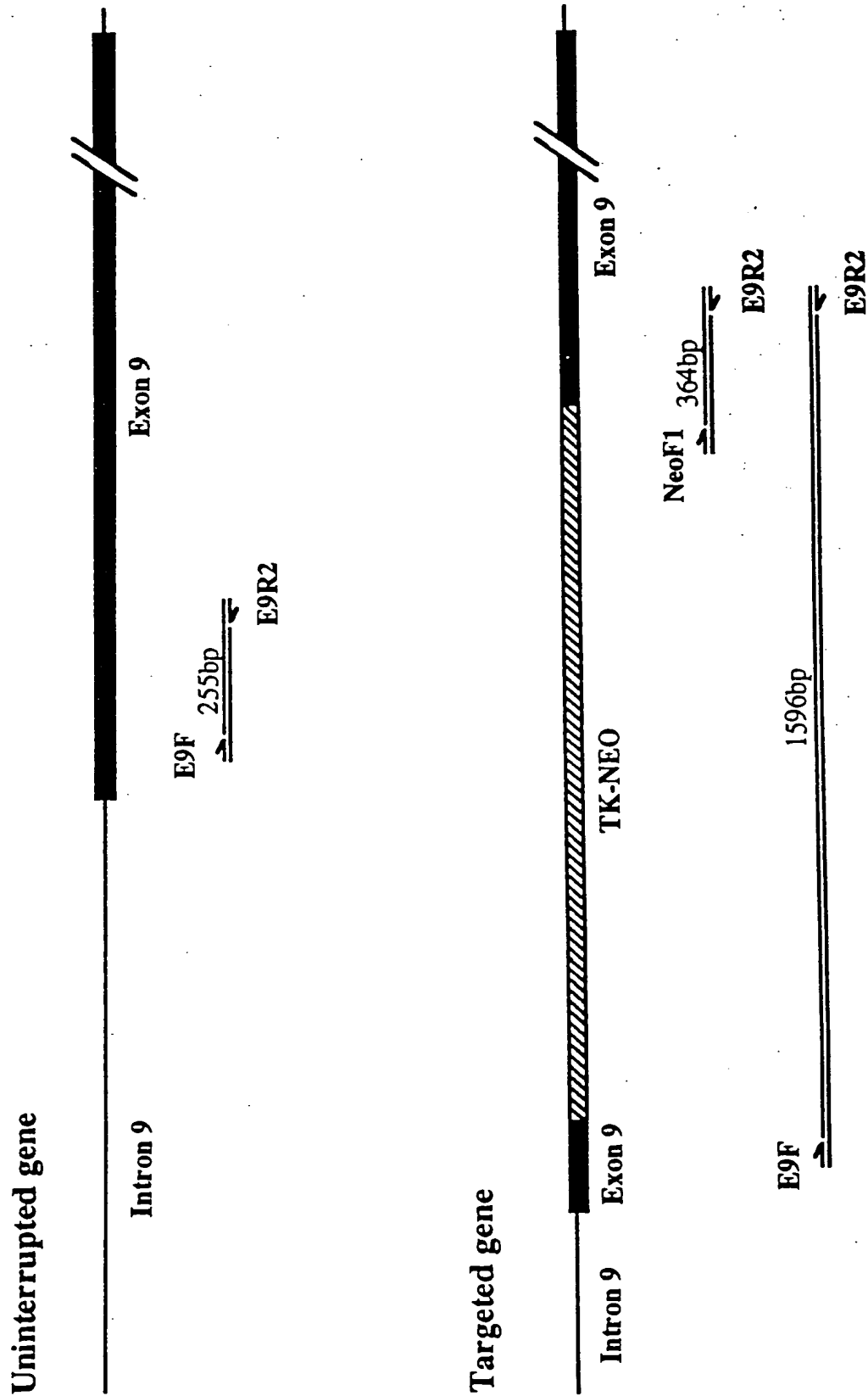


FIG. 2I

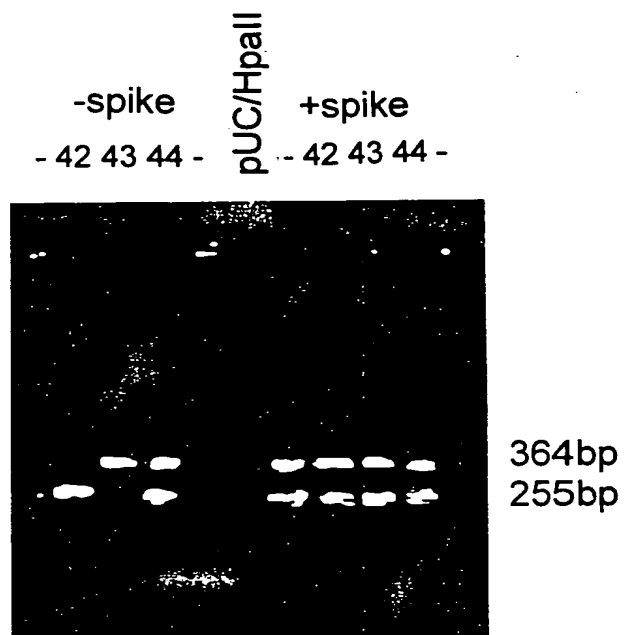
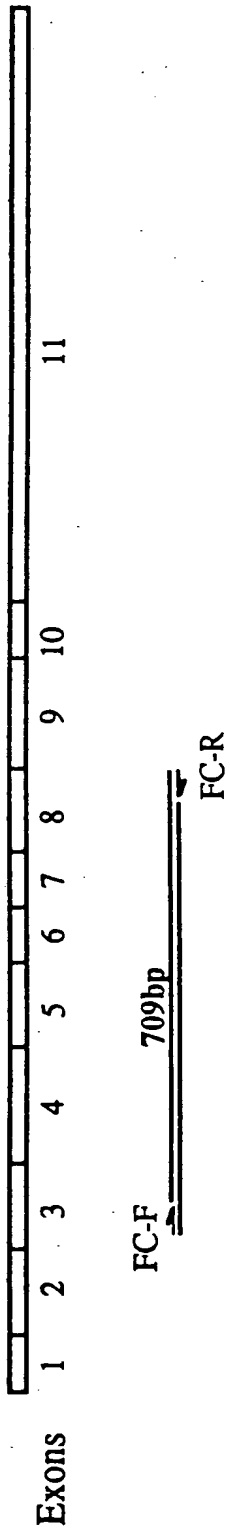


FIG. 22

Primer binding sites within mouse ferrochelatase cDNA



Primer binding sites within mouse α -1,3-GalT cDNA

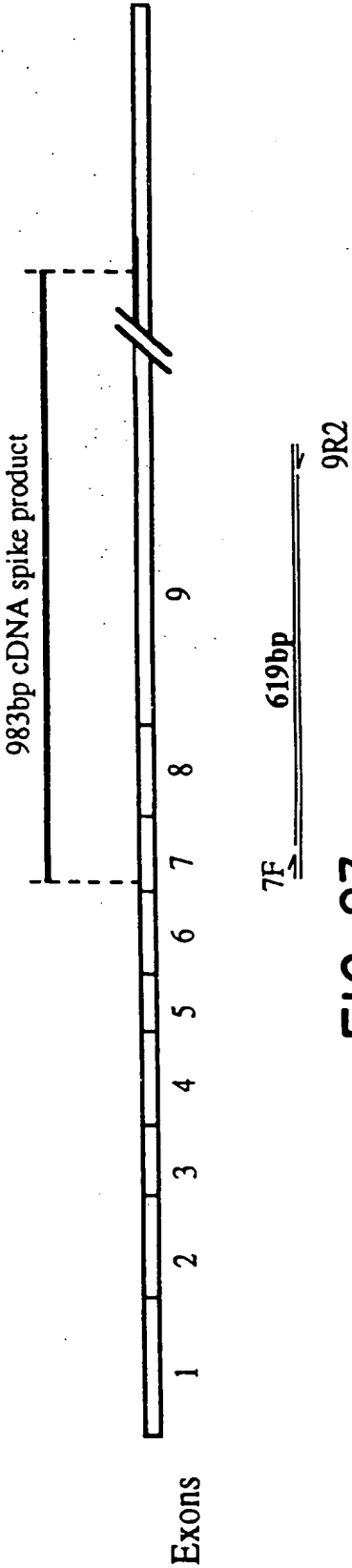
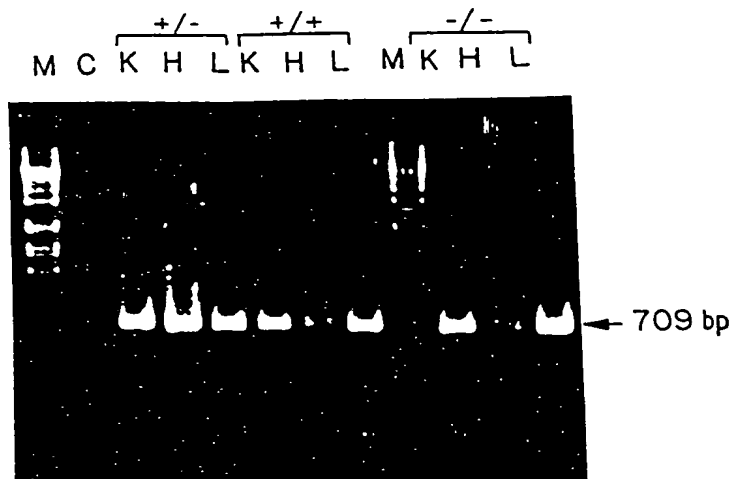


FIG. 23

i) Ferrochelatase, FC-F/R

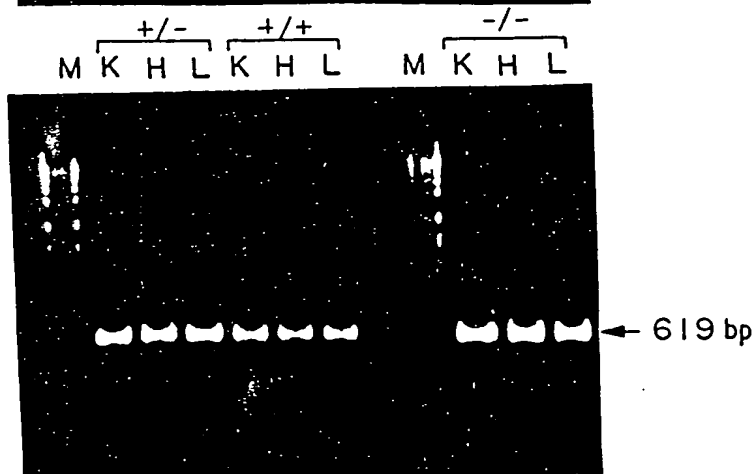
M, Marker SPP-I
C, MQW control
K, KIDNEY
H, HEART
L, LIVER

FIG. 24a



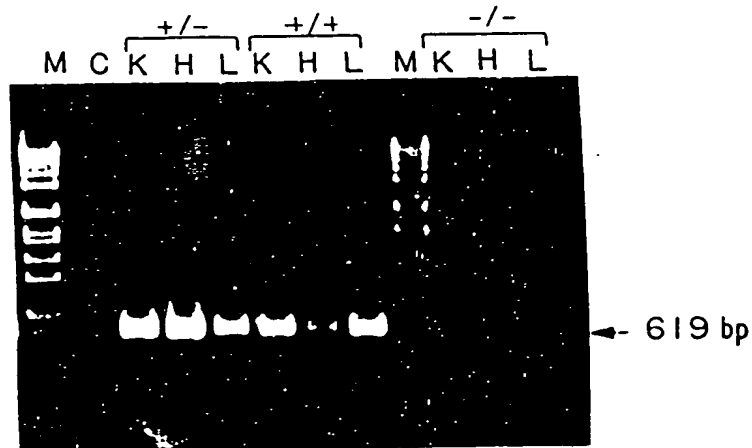
ii) α -1,3-GT cDNA spike
+ 7F/9R2 primers

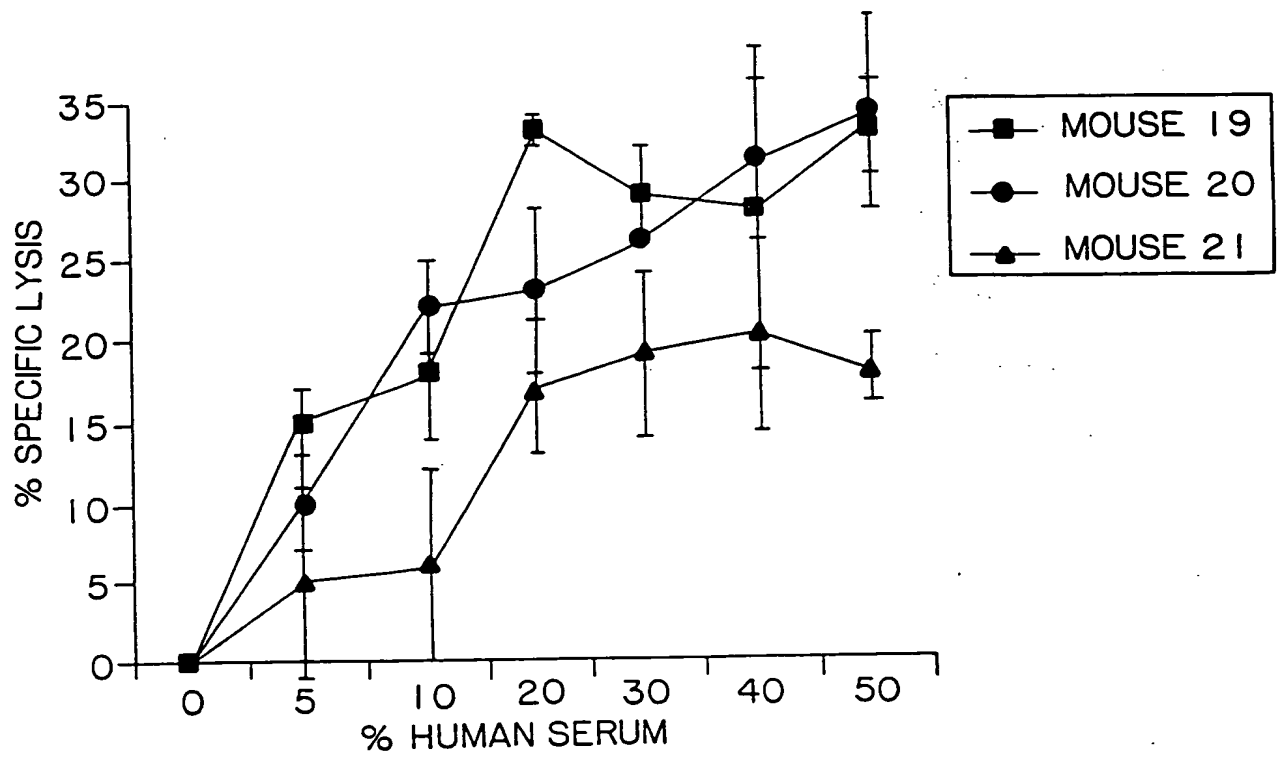
FIG. 24b



iii) α -1,3-GT
7F/9R2 primers

FIG. 24c





MOUSE 19: WILD TYPE; MOUSE 20: HETEROZYGOTIC Gal KO; MOUSE 21:
HOMOZYGOUS Gal KO

FIG. 25

T-LIF SEQUENCE - Murine

CTGACACCTTTTCGCTTTCTCTTGCGTGTCCGCCTGCGACCTTTCCCCACCCC

GGCCTCTTTCCTGGTTGCACCACTTCTCTCATTCCAAAGGATTGTGCCCTTA

CTGCTGCTGGTTCTGCACTGGAAACACGGGGCAGGGAGCCCTCTTCCCATCAC

CCCTGTAAATGCCACCTGTGCCATACGCCACCCATGCCACGGCAACCTC

Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly
ATG AAC CAG ATC AAG AAT CAA CTG GCA CAG CTC AAT GGC

Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly
AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA GCT CAA GGX

Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro Asn
GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT AAC

Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys
ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG

Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser
ACC AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC

Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
GCC TCC CTG ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC

Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile
CCC ACT GCC GTG AGC CTC CAG GTC AAG CTC AAT GCT ACT ATA

Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu
GAC GTC ATG AGG GGC CTC CTC AGC AAT GTG CTT TGC CGT CTG

Cys Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val
TGC AAC AAG TAC CGT GTG GGC CAC GTG GAT GTG CCA CCT GTC

Pro Asp His Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu
CCC GAC CAC TCT GAC AAA GAA GCC TTC CAA AGG AAA AAG TTG

Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser Val
GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT GTG

Val Val Gln Ala Phe ***
GTG GTC CAG GCC TTC TAG AGAGGAGGTCTTGAATGTACCATGGACTG...

FIG. 26

HUMAN T-1 IF SEQUENCE

```

GACCTTTTGC CTTTCTCTC TCCTGGTGCA CCATTCCTC TCCCTCCCTG 50
AGCCGGAGTT GTGCCCCTGC TGTGTTTCT GCACTGGAAA CATGGGGCGG 100
GGAGCCCCCT CCCCATCACC CCTGTCAACG CCACCTGTGC CATACGCCAC 150
CCATGTCACA ACAACCTC ATG AAC CAG ATC 182
Met Asn Gln Ile
AGG AGC CAA CTG GCA CAG CTC AAT GGC AGT GCC AAT GCC CTC 227
Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu
5 10 15
TTT ATT CTC TAT TAC ACA GCC CAG GGG GAG CCG TTC CCC AAC 272
Phe Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn
20 25 30
AAC CTG GAC AAG CTA TGT GGC CCC AAC GTG ACG GAC TTC CCG 317
Asn Leu Asp Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro
35 40 45
CCC TTC CAC GCC AAC GGC ACG GAG AAG GCC AAG CTG GTG GAG 362
Pro Phe His Ala Asn Gly Thr Glu Lys Ala Lys Leu Val Glu
50 55 60
CTG TAC CGC ATA GTC GTG TAC CTT GGC ACC TCC CTG GGC AAC 407
Leu Tyr Arg Ile Val Val Tyr Leu Gly Thr Ser Leu Gly Asn
65 70
ATC ACC CGG GAC CAG AAG ATC CTC AAC CCC AGT GCC CTC AGC 452
Ile Thr Arg Asp Gln Lys Ile Leu Asn Pro Ser Ala Leu Ser
75 80 85
CTC CAC AGC AAG CTC AAC GCC ACC GCC GAC ATC CTG CGA GGC 497
Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile Leu Arg Gly
90 95 100
CTC CTT AGC AAC GTG CTG TGC CGC CTG TGC AGC AAG TAC CAC 542
Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr His
105 110 115
GTG GGC CAT GTG GAC GTG ACC TAC GGC CCT GAC ACC TCG GGT 587
Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly
120 125 130
AAG GAT GTC TTC CAG AAG AAG AAG CTG GGC TGT CAA CTC CTG 632
Lys Asp Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu
135 140
GGG AAG TAT AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC 677
Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe
145 150 155
TAG CAGGAGGTCT 722
***

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FIG. 27

FIG. 28

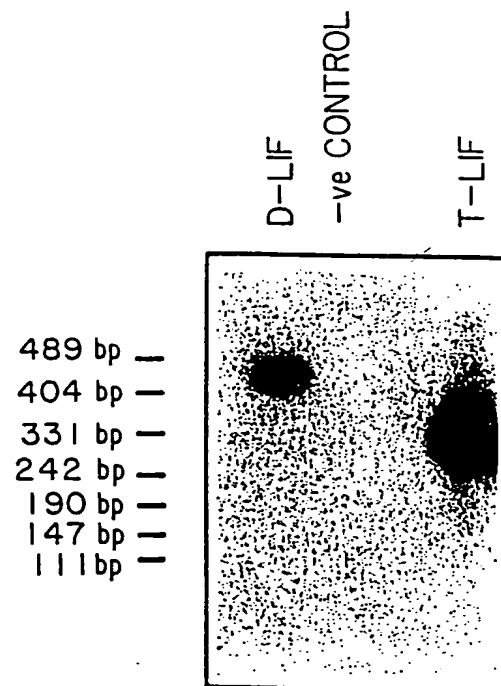
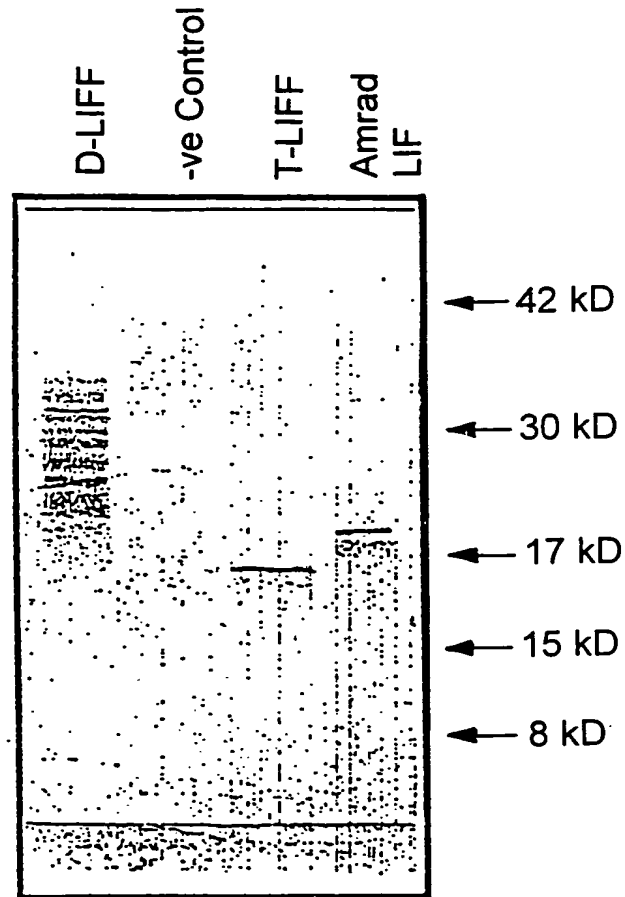
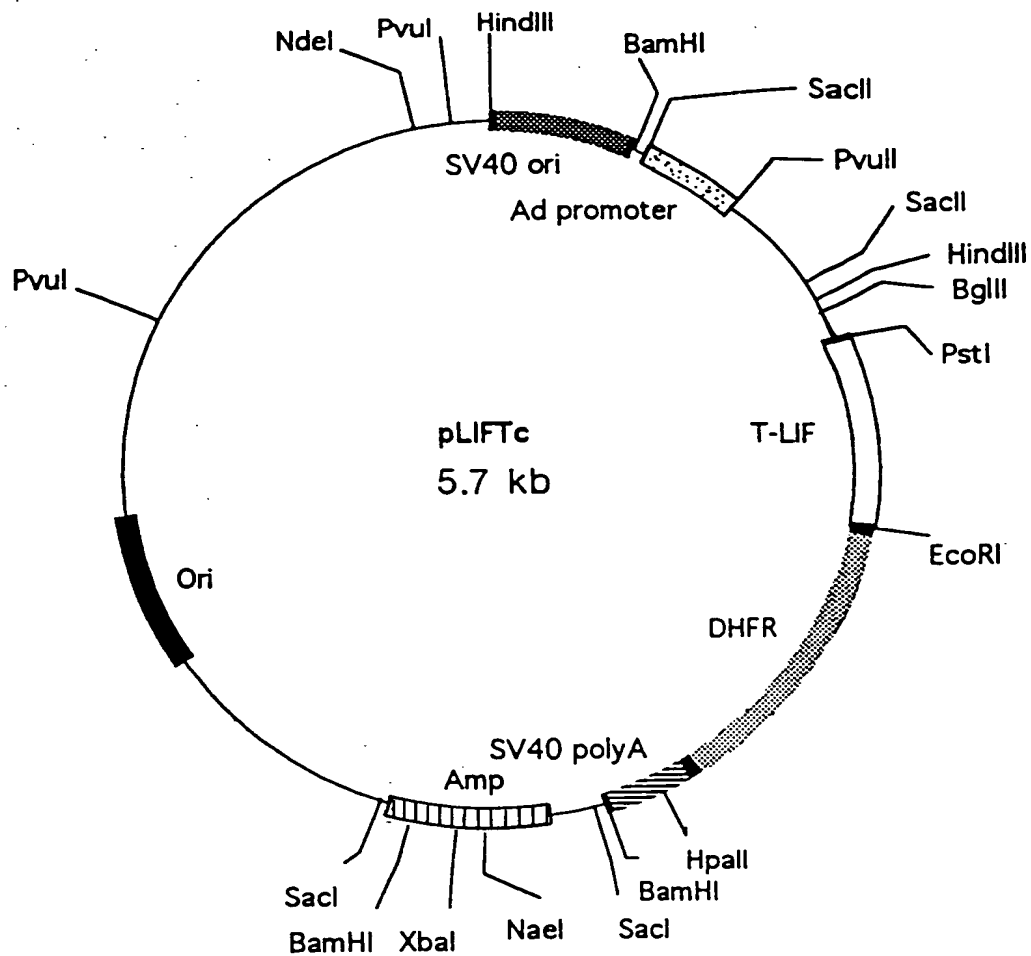


FIG. 30








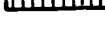
-  Dihydrofolate reductase 3' end
-  Adenovirus promoter
-  SV40 origin of replication
-  T-LIF coding region
-  Bacterial origin of replication
-  Ampicillin resistance gene

FIG. 29